4/2/03

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25 354 66.2 155 5 AAU900993 26 354 66.2 155 5 AAU900999 27 354 66.2 155 9 ADX08371 28 352.5 65.9 159 5 AAU900998 29 352.5 65.9 159 9 ADX08376 31 347 64.9 147 2 AAW18158 32 347 64.9 149 2 AAW18159 34 347 64.9 149 2 AAW18156 35 347 64.9 149 2 AAW18156 36 347 64.9 149 2 AAW18156 37 347 64.9 149 2 AAW18156 38 347 64.9 149 2 AAW18156 39 347 64.9 149 2 AAW18159 30 347 64.9 149 2 AAW18159 31 347 64.9 149 2 AAW18159 32 347 64.9 149 8 ADL18366 34 347 64.9 149 8 ADL18366 34 347 64.9 149 8 ADL18366 35 340.5 63.6 160 9 ADX08378 36 340.5 63.6 160 9 ADX08378 37 A40.5 63.6 160 9 ADX08378 38 ADD1705 BOWINE pe	ALIGNMENTS RESULT 1 ADJ82974	4 4 0 2 200 2 2	Discource; Page 22-93; Discource per per per per per per per per per pe
GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen Ltd. OM protein - protein search, using sw model Run on: January 12, 2006, 21:41:48; Search time 53.6679 Seconds (without alignments) 826.886 Million cell updates/sec Title: US-10-815-562-2_COPY_31_131 826.886 Million cell updates/sec Title: US-10-815-562-2_COPY_31_131 Sequence: 1 QVLSYKEAVLRAIDGINQRSVTLNQARGSFDISCDKDNKR 101 Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5 Searched: 2443163 seqs, 439378781 residues Total number of hits satisfying chosen parameters: 2443163	Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0* Maximum Match 100* Listing first 45 summaries	eq_21:* Beqp1990B:* Beqp2000B:* Beqp2001B:* Bedp2001B:* Bedp2001B	Pesult Core Match Length DB ID Description

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a polypeptide encoded by one of a large number of 5' ESTB derived from mRNAB encoding secreted proteins. The 5' ESTB were prepared from total human RNAB or polyA+ RNAB derived from 30 different tisques. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTB are not well suited for isolating cDNA primed cDNA libraries such 5' ends of mRNAB and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTB are derived from mRNAB with intact 5' ends and can therefore be used to obtain full length cDNAB and genomic DNAB: 5' ESTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
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                                                                                                                                                                                                                                                                                                                                                                                                    expressed sequence tag; secreted protein; cDNA isolation;
                                                                                QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTWDGDPDTPKPVSFTVKETVCPRTT
                                                          QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; SEQ ID NO 7862; 71pp + Sequence Listing; English.
                         Indels
                                                                                                                                                     QQSPEDCDFKQDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
                                                                                                                                61 QOSPEDCDFKXDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
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100.0%; Pred. No. 1.1e-56;
ive 0; Mismatches 0;
         9.6e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duclert A, Giordano J;
100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein, SEQ ID NO: 7862
                                                                                                                                                                                                                                                        AAG03781 standard; protein; 152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; chromosome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0122487P
                                                                                                                                                                                                                                                                                                                                (first entry)
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Matches 101; Conservative
                         Matches 101; Conservative
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N-PSDB; AAC03787.
         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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The invention relates to a novel polypeptide composition for preventing disease in an organism which comprises one or more types of polypeptide which have an alpha-helix structure and/or thionine component. The composition of the invention demostrates antibacterial and antifugal activities and may be useful for preventing a disease in an organism, for generating cultivated plants and in providing resistance to plant tissue against fungi such as Pyrtcularia oryzae (rice blast fungus), caratocystis fimbriata and bacteria such as Peseudomonas etc. The composition has high antimicrobial activity at low concentration. The current sequence is that of the rabbit CAP18 full-length protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial polypeptide composition for a plant pathogen, comprises one or more types of thionine and/or a polypeptide having an alpha helix structure, as an active ingredient.
                                                                                                                                                                                                                       alpha-helix; thionine; antibacterial; antifungal; plant;
fungi resistance; rice blast fungus; Ceratocystis fimbriata; bacteria;
Pseudomonas; antimicrobial; rabbit; CAP18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 OVLSYKBAVLRAIDGINORSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKBTVCPRTT
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94 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 535; DB 8;
Pred. No. 1.2e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (TOYW ) TOYOTA CHUO KENKYUSHO KK.
                                                                                              ADK70797 standard; protein; 169
                                                                                                                                                                                            Human CAP18 full-length protein.
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                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                               ADK70797;
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AAR92924
ID AAR;
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AC AAR;
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Gaps

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Indels

61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101

1 OVLSYKBAVLRAIDGINORSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT

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The present sequence represents a human cationic protein, having lipopolysaccharide binding and anticoagulant activity. The polypeptide idesignated CAPIS. Amino acids 134-170 of CAPIS represent a reactive nitrogen inhibitory protein (RNIP). The CAPIS polymclectide is useful for producing cationic proteins. The CAPIS polypeptide is useful for treating and diagnoshing lipopolysaccharide-associated conditions such as gram negative sepsis, and/or coagulation-related disorders, such as disseminated intravascular coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine, cathelicidin, antimicrobial, immunostimulant, immune response, antigen presenting cell, adjuvant, human, antibiotic, {\it FALL}-39.
                                                                                                                                                                                                                                                                                               Novel human cDNA encoding cationic proteins having lipopolysaccharide binding and anticoagulant activity, useful for treating and diagnosing gram negative sepsis and disseminated intravascular coagulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
/note= "reactive nitrogen inhibitory protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 535; DB 3; Length 170; 100.0%; Pred. No. 1.2e-56; tive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human peptide antibiotic FALL-39 precursor sequence.
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                                                                                                                                                                                                                            Hirata M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB07707 standard; peptide; 170
                                                                                                           92US-00916761.
92US-00916765.
93WO-US006731.
94US-00313681.
96US-00691280.
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                                                                                  99US-00322911
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                                                                                                                                                                                                (PANO-) PANORAMA RES INC.
                                                                                                                                                                                                                           Larrick JW, Wright SC,
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                                                                                                                                                                                                                                                                    N-PSDB; AAA59574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 170 AA;
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                           US6103888-A.
                                                                                01-JUN-1999;
                                                      15_AUG-2000.
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                                                                                                                           17-JUL-1992)
15-JUL-1993;
                                                                                                                                                                    01-AUG-1996;
                                                                                                              17-JUL-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, cationic protein, lipopolysaccharide binding; anticoagulant;
CAP18; reactive nitrogen inhibitory protein; RNIP; gram negative sepsis;
coagulation-related disorder; disseminated intravascular coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 535; DB 2; Length 170; 100.0%; Pred. No. 1.2e-56; tive 0; Mismatches 0; Indels
                             FALL-39; cathelin; antibiotic; antimicrobial; antibacterial.
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                                                                                                 1. .131
/label= Prepro-peptide
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                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                   resistance and is non-cytotoxic.
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                                                                                                                           132. .170
/label= FALL-39
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 Prepro-FALL-99
                                                         Homo sapiens
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Matches
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preservation of organs prior to transplant.
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Matches 101; Conservative
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VON DEGENPELD
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N-PSDB; ADF18220.
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Misc-difference
                                                                                                                                                                                                                                                                                                                                              Sequence 170 AA;
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(KOCZ/) KOCZULLA
(VDEG/) VON DEGE
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                                                                                                                                                                                                 The invention relates to a vaccine comprising at least one antigen and at least one cathelicidin derived antimicrobial peptide or its derivative. The vaccine is useful for active immunication, especially of humans or animals without protection against the specific antigen. The cathelicidin derived antimicrobial peptide is useful in the preparation of an adjuvant for enhancing the immune response to at least one antigen, where the adjuvant enhances the uptake of at least one antigen, where the presenting cells (APC), and the adjuvant is added to the vaccine. Sequences ABB07701-07 represent cathelicicidin proteins form various
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Media comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds useful for the storage and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                       Vaccine for active immunization or for preparing an adjuvant for enhancing an immune response to at least one antigen, comprises at least one antigen and at least one cathelicidin derived antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVLSYKEAVLRAIDGINQRSSDANLYRLLDDDPRPTMDGDPDTPKPVSFTVKETVCPRTT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transplant; antimicrobial peptide; pore forming agent; cardioplegia; cell surface receptor binding compound; kidney transplant; cardioplegia; organ transplant; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          QSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transplant media associated antimicrobial peptide #32
                                               Egyed A;
                                               Buschle M,
              (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU90996 standard; peptide; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcanulty JF;
                                                                                                                                                                       Disclosure, Fig 1; 65pp; English
                                             Zauner W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000US-0221632P.
17-NOV-2000; 2000US-0249602P.
15-MAY-2001; 2001US-0290932P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUL-2001; 2001WO-US023785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 101; Conservative
                                             Mattner F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy CJ, Reid TW,
                                                                            WPI; 2002-269154/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-268995/31.
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MURP/) MURPHY C J.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200209738-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31
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                                             Pritz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
                                                                                                                                                                                                                                                                                                                                               species
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
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The invention describes new transplant compositions comprising antimicrobial polypeptides or pore forming agents and/or cell surface antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds. The media is capable of extending the preservation period past 72 hours and can provide organs with increased functionality upon transplant, animals receiving kidneys stored in the receiving kidneys stored in the creatinine levels of less than half of those observed in control animals receiving kidneys stored in UW solution (defined in the specification) alone. Lower serum creatinine levels are indicative of healthier kidneys alone. Lower serum creatinine levels are indicative of healthier kidneys and a more preferable prognosis for the transplant patient. The media of the incidence and/or severity of delayed graft function in patients receiving transplant of healthier conjans leads to a decrease in chronic rejection. This sequence represents an antimicrobial peptide studied in the development of the transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTWDGDPDTPKPVSFTVKETVCPRTT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 535; DB 5;
100.0%; Pred. No. 1.2e-56;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Encoded by AAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Von Degenfeld G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
Disclosure; Page 27; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADF18219 standard; protein; 170 AA.
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profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and

Disclosure, Page, 56pp, English

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The present invention is based on the finding that human antimicrobial peptide LL-37 ADF18218 is capable of inducing functionally important angle in cell culture and in vivo by activation of the receptor molecule FPRALI. LL-37 can be used in the preparation of a pharmaceutical composition for the prevention or treatment of a disease caused by, or resulting in, a reduced level of anglogenesis or arteriogenesis, or for the treatment of (infected) wounds or cancer. The disease may be associated with reduced blood flow, such as atherosclerosis, coronary heart disease, stroke, arterial occlusive disease or an ulcer.

The disease of anglogenesis through inhibition of IL-37 can be used to treat tumours, especially a carcinoma or sarcoma including cancer of the bile duct, brain, breast, colon, stomach, male and female reproductive corgans, lung and airways, skin, gallbladder, liver, nasopharynx, nerve cells, kidney, prostate, and Kaposi's sarcoma (all claimed). The present protein sequence is not explained in the specification.
9e of a peptide LL-37 for the preparation of a composition for
reventing or treating wounds or a disease caused reduced blood flow,
g. atherosclerosis, coronary heart disease, stroke, arterial occlusive
                                                                                                                                               Disclosure; Page; 15pp; English.
                                                                                           diseases or ulcer.
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Sequence 170 AA;

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                                                                                       QVLSYKEAVLRA I DGINQRSSDANLYRLIDLDPRPTMDGDPDTPKPVSFTVKBTVCPRTT
                                                                  QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                    Gaps
                                    ö
Length 170;
                                0; Indels
                                                                                                                                                     91 QOSPEDCDFKCGGLVKRCMGTVTLNQARGSFDISCDKDNRR 131
                                                                                                                                  61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
100.0%; Score 535; DB 7;
100.0%; Pred. No. 1.2e-56;
iive 0; Mismatches 0;
                  Best Local Similarity 100.
Matches 101; Conservative
   Query Match
Best Local Similarity
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ADP65263 standard; protein; 170 AA 12-AUG-2004 ADP65263;

Human cathelicidin antimicrobial peptide. 🗸 (first entry)

rheumatoid arthritis; collagen-induced; Immunosuppressive; antirheumatic; antiarthritis; osteopathic; antigout; antiinflammatory; dermatological; immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis; autoimmune disease; arthritide; gene expression analysis; immune; human

Homo sapiens

WO2003072827-A1. 04-SEP-2003.v 31-OCT-2002; 2002WO-US035433.

(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

31-OCT-2001; 2001US-0336220P

Thorton SL

WPI; 2003-712740/67. Hirsch R,

GENBANK; NP_004336.

Diagnosing and analyzing autoimmune disease using gene expression

22-JUL-2002; 2002JP-00213040. 14-MAR-2003; 2003JP-00070932. 22-JUL-2003; 2003WO-JP009267.

29-JAN-2004.

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The results in a give expression signature of the mark, and using that gene expression signature to diagnature to the manual contains the authorization of a the gene expression of at least 60% of the genes comprises; a treatment of the gene signature. The invention of further comprises; a treatment of rheumatoid arthritis in a mammal of the mouse; diagnosis of rheumatoid arthritis in a mammal of the context than a mouse; diagnosis of rheumatoid arthritis in a mammal, and array or gene chip, specific for rheumatoid arthritis; screening the candidate drug in vitro for the treatment of collagentinduced arthritis; and reducing the symptoms associated with collagentinduced arthritis; and reducing the symptoms associated with collagentinduced arthritis. The compositions of the invention have the following artifocut, antifilammatory, dermatological, and immunomdulatory. The methods and compositions of the present invention are useful for theumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, cheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, immune disease caused by an infectious agent. This sequence reparting to the genes used in the analysis and treating to the genes used in the analysis and treating to the genes used in the analysis and treating to the genes used in the analysis and treatment of autoimmune disease or arthritides. Not shown in the specification. It has been supplied in an electronic format from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                      The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 QVLSYKEAVLRAIDGINQRSSDANLYRLLDDDPRPTMDGDPDTPKPVSFTVKETVCPRTT 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAP18; cationic antimicrobial protein of 18 kDa; bacterial pneumonia; chronic lung disease; acute lung disease; inflammatory lung disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 QQSPEDCDFRCCGLVRRCMGTVTLNQARGSFDISCDKONRR 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 535; DB 7; 100.0%; Pred. No. 1.2e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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ARDS; bronchial asthma; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004009640-A1.
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WPI; 2004-364936/34.
N-PSDB; ADN41826.
                                                                                                                                                                                                                                                                          Sequence 170 AA;
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WO2004005338-A1
                                                                                                        Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                    Local Simi
hes 101;
                   15-JAN-2004
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Matches
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                                                                                                                The present invention relates to a novel CAP18 (cationic antimicrobial protein of 18 kDa) antibody that can bind with human CAP18 peptide fragments ADI29579-ADI29581. The antibody is useful in reagents and kits for the detection, diagnosis and monitoring bacterial pneumonia and other CAP18-related diseases like chronic and acute lung diseases, inflammatory
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                                                                                                                                                                                                                                                                  QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 90
                                                        * antibody against an antibacterial peptide, particularly human CAP18,
plicable in reagents and kits for detection, diagnosis and monitoring
bacterial pneumonia.
                                                                                                                                                                  diseases, ARDS and bronchial asthma. The present sequence is human
                                                                                                                                                                                                                                                       OVLSYKEAVLRAIDGINORSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          pep714-related peptide; precursor; human; secreted peptide; Pep714; oral mucositis; oral lesion; cystic fibrosis; respiratory infection;
                    Hashimoto
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                Length 170
                   Ishizaka A,
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "dibasic peptidase cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "dibasic peptidase cleavage site"
                                                                                                                                                                                                                                                                                            QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
                                                                                                                                                                                                                                                                                                        QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= antibacterial_protein_FALL-39
134. .170
/label= antibacterial_protein_LL-37
                                                                                                                                                                                                                                                                                                                                                                                                                        Human Pep714-related peptide precursor SEQ ID NO: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "dibasic peptidase cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "dibasic peptidase cleavage
151. .152
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                               100.0%; Score 535; DB 8;
100.0%; Pred. No. 1.2e-56;
ive 0; Mismatches 0;
                   Tamura H,
                                                                                               Disclosure; SEQ ID NO 4; 52pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l. .30
/label= Bignal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               ADJ82973 standard; protein; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= propeptide
106. .107
                  Naiki Y,
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140. .141
                                                                                                                                                                                                                          Best Local Similarity 100. Matches 101; Conservative
                   Toyooka K,
(SEGK ) SEIKAGAKU CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note
                                      WPI; 2004-143269/14
                                                                                                                                                                                              Sequence 170 AA;
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                                                                  applicable
of bacteria
                  Kirikae T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumonia
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                                                                                                                                                                                                                 Query Match
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The present invention relates to a Pep714-related peptide. This is useful for inhibiting microbial propagation, preferably viral propagation, and in the treatment of chemotherapy and radiotherapy induced oral mucoaltis, oral lesion, ventilator associated pneumonia, chronic respiratory infections and cystic fibrosis. The present sequence is a Pep714-related peptide precursor protein shown in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                         Novel Pep714-related polypeptide having biological activity, useful for treatment and prevention of microbial or viral infection, cystic fibrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection, cathelicidin type peptide; LL-37; antimicrobial;
antiinflammatory; immunostimulant; bacterial infection; neutropenia;
toothpaste; mouthwash; gingivitis; oral infection; periodontitis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPPRPTMDGDPDTPKPVSFTVKETVCPRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                  Niknejad A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 91-92; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          and chronic respiratory infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Puetsep K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADN41827 standard; protein; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human LL-37 protein SEQ ID NO:2.
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30-JUN-2003; 2003WO-EP006930
                                                          08-JUL-2002; 2002US-0394486P
07-JAN-2003; 2003US-0438602P
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                                                                                                                                                                                                                     Jeandenans
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                                                                                                                                                       (GENE-) GENEPROT INC
                                                                                                                                                                                                                                                                               WPI; 2004-099371/10.
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The present invention describes a method for determining the susceptibility of a subject to infection. The method comprises: (i) providing a sample from a subject; (ii) detecting any cathelicidin type providing a sample from a subject; (ii) detecting any cathelicidin type captibility of the sample; (iii) optionally comparing the susceptibility of the subject to infection (where no LL-37 or a low level of LL-37 indicates that subject is susceptible to infection; and (v) determining the susceptibility defining the subject is susceptible to infection. Also optionally administering an antimicrobial agent to reduce infection. Also corticosteroid or growth factor (preferably recombinant granulocyte colony stimulating factor (G-CSF) or GM-CSF). The product has attimicrobial, antilifanmatory and immunostimulant activities. The method can be used for determining the susceptibility of a subject to infection such as bacterial infection (e.g. Actinobacillus catinomycetemcomitans infection) and neutropenia, and for diagnosing neutropenia (e.g. Kostmann morbus). The method is also useful in the manufacture of a medicament in the form of toothpaste or mouthwash for the preventative treatment of infection e.g. gingivitis, oral infection (such as periodontitis), and for the areament of neutropenia. The method controls the normal flora in neutropenia and so combat infections. The present sequence represents the proform of human LL-37, which is used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evaluating cystic pulmonary fibrosis, by measuring cationic antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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            Determination of susceptibility of subject to infection comprising detecting cathelicidin type peptide present in sample, optionally comparing level of peptide in sample to control sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cystic pulmonary fibrosis; cationic antimicrobial protein; CAP18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 535; DB 8;
100.0%; Pred. No. 1.2e-56;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cationic antimicrobial protein-18.
                                                                                                   Disclosure; SEQ ID NO 2; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR47315 standard; protein; 170 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-FEB-2004; 2004JP-00036471
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Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pulmonary disease.
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The invention relates to a novel method for evaluating cystic pulmonary fibrosis. The method comprises: measuring the quantity of cationic attimicrobial protein of 18 kps (CAP18) in the biological sample collected from the individual; comparing the quantity of CAP18 measured in the previous step and the quantity of CAP18 in a control sample; and contained results. The invention further comprises: a kit for carrying out the evaluating method, comprising a solid-phase component and an antibody coupled with an antigenic peptide having a sequence of ADR47312, or a colld-phase component comprising a solid-phase component comprising an solid-phase component comprising an immobilised antibody (first antibody) which is coupled with the antigenic peptide. The method or kit are antibody) coupled with the antigenic peptide. The method or kit are useful for evaluating cystic pulmonary fibrosis for the presence or absence of a risk of cystic pulmonary fibrosis, evaluation of serious or acute conditions, or the evaluation of the advanced grade of the disease. The method accurate evaluation of the acute or serious conditions, or the evaluation of the acute or serious conditions, or the cypie pulmonary diseases. This sequence represents the human condition.
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protein of 18 kDa (CAP18) quantity in biological sample, and evaluating fibrosis by comparing measured quantity and quantity of CAP18 in control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSPTVKBTVCPRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target, TAT; human; overexpression; ctumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; lurer cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 535; DB 8;
Pred. No. 1.2e-56;
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                                                                               Disclosure; SEQ ID NO 4; 14pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 170 AA;
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                                              gample.
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ID ABME
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(EURO-) EUROSCREEN SA.

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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide perves as least 80% identical to the TAT nucleic acids and polypeptide polypeptides expression vectors and host cells compitating a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or aliagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, inverse system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide.
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                                                                                                                                        New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.
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                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; SEQ ID NO 1129; 7273pp; English.
WPI; 2004-347921/32.
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Best Local Similarity
                                             N-PSDB; ACN37923
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gene therapy; diagnosis; cell signaling; gene therapy; lymphoproliferative disease; dermatological disease; dermatological; demostatic; inflammation; antiinflammarory; hematological disease; immune disorder; neoplasm; cardiovascular-gen.; cns-gen.; neoplasm; cardiovascular-gen.; cns-gen.; neoplasm; cardiovascular-gen.; cns-gen.; chemerin.
                                                                                                                                                                                                                                                                                                                                                                                                             91 QQSPEDCDFRGDGLVRRCMGTVTLNQARGSFDISCDKDNRR 131
                                                                                                                                                                                                                                                                                                                                                  61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADW43827 standard; peptide; 170 AA.
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Matches 101; Conservative
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ADW43827
ID ADW43
XX
XX
AC ADW43
XX
DT 24-MA
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XX
MW Gene
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MW Hemosh
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91 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 131

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Search completed: January 12, 2006, 21:48:09 Job time : 53.6679 secs

25-JUN-2004; 2004WO-EP006945. 25-JUN-2003; 2003US-00603566

WO2005000875-A2

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The invention describes a polypeptide (I) of up to 50 amino acids where the polypeptide binds specifically to a chemerink polypeptide. Also described are: a mucleic acid sequence encoding (I); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal transferted with the expression vector; a (therapeutic) composition and isolated Chemerink polypeptide or a nucleic acid acquence of (I); an anibody that selectively binds to (I); identifying an agent that modulates the interaction between a Chemerin polypeptide and agent that modulates the interaction between a Chemerin polypeptide and agent that modulates the interaction between a Chemerink polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a Chemerink polypeptide of the function of Chemerink polypeptide; detecting the presence, in a sample, of an agent that modulates the function of Chemerink polypeptide is detecting the presence, in a sample, of an agent that modulates the function of Chemerink polypeptide of a ganaling; a kit, for screening agents that modulates the function of Chemerink polypeptide of signaling; a kit, for screening agents that modulates the signaling activity of Chemerink polypeptide of control of the signaling activity of Chemerink polypeptide of signaling; a kit, for acreening agents that the signaling activity of chemering polypeptide of composition or activity of chemering polymeraced with a polymelectide encoding (I), an isolated polymelectide encoding (I), and its packaging creamedicanent for a vivo gene therapy or for in vivo gene therapy or a medicament for a vivo gene therapy or for in vivo gene therapy or a medicament for a vivo gene therapy or for in vivo gene therapy or gene therapy or gene therapy or a medicament for a vivo gene therapy or for in vivo gene therapy or gene therapy or gene polymerical cament as paraproclaments, purpura, sarcoldosis, Sezary Syndrome, Waldenstron's Macroglobulinemia, Gaucher's bisease, histlocytosis, and any other w
                                                                                                                                                            New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstron's Macroglobulinemia, Gaucher's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                            Loison C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 535; DB 9; Length 170; 100.0%; Pred. No. 1.2e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                            Parmentier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                      Example 2; SEQ ID NO 51; 183pp; English.
                                            Detheux M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             processing of immature chemerin.
                                                                                                                                                                                                                                      Disease, or histiocytosis.
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Matches 101; Conservative
                                            Wittamer V, Communi D,
                                                                                                                  WPI; 2005-058121/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 170 AA;
                                                                     Ooms FDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
셤
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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

January 12, 2006, 21:43:14 ; Search time 8.94465 Seconds (without alignments) 1086.448 Million cell updates/sec Run on:

US-10-815-562-2_COPY_31_131

1 QVLSYKEAVLRAIDGINQRS.....VTLNQARGSFDISCDKDNKR 101 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	QI	Description
-	535	100.0	170	2	138932	CAP18 precursor -
8	530	99.1	170	~	S74248	antibacterial pept
٣	366	68.4	155	~	S68229	antimicrobial pept
4	361	67.5	153	8	A53421	
2	354	66.2	155	7	S27018	Ψ.
y	350	65.4	172	7	S68232	
7	350	65.4	212	7	S57330	like
80	347	64.9	147	N	0060NL	protegrin 2 precur
o	347	64.9	149	~	A53895	m
10	347	64.9	149	7	S57607	Н
11	347	64.9	149	~	B53895	4
12	347	64.9	149	~	S57609	
13	346	64.7	228	~	S40463	prophenin (PF-2) p
14	344	64.3	166	N	S41731	antibacterial prot
15	343	64.1	171	7	JQ1171	18K lipopolysaccha
16	340.5	63.6	152	7	S68411	cathelin-related p
17	340	63.6	167	~	S68967	antibacterial pept
18	340	63.6	176	~	A45328	-
19	333.5	62.3	160	7	S68412	cathelin-related p
20	333.5	62.3	160	7	S68228	myeloid antimicrob
21	327	61.1	173	~	870521	cathelin-related p
22	323	60.4	144	н	JC1222	din precu
23	319	59.6	96	-	XKPGC	cathelin - pig
24	312	58.3	190	~	S68230	antimicrobial pept
25	146	27.3	135	~	B46634	polymorphonuclear
26	4	26.9	137	N	A46634	polymorphonuclear
27	85.5	16.0	200	0	146051	secreted phosphopr
28	82	15.9	434	-	KGBOL2	
59	85	15.9	619	Н	KGBOH2	kininogen, HMW II

kininogen, LMW I p kininogen, HMW I p	hypothetical prote probable cysteine	<pre>spp-24 precursor - photosystem II oxy</pre>	conserved hypothet	photosystem II oxy	photosystem II oxy	kininogen, LMW pre	kininogen, HMW pre	photosystem II oxy	major surface glyc	fragile X mental r	hypothetical prote	photosystem II oxy
KGBOL1 KGBOH1	C84397 T05390	G01654 S16586	G82903	804132	T02066	KGHUL1	KGHUH1	T08403	JC2217	860173	G87536	S11852
	N N	0 0	7	N	N	-	ч	N	~	N	~	N
436	263 355	211	364	329	332	427	644	331	1076	673	312	332
15.7	14.8 13.6	13.6 13.6	13.4	13.0	13.0	12.9	12.9	12.8	12.8	12.7	12.4	12.4
8 4 4 4	79 73	72.5	71.5	69.5	69.5	69	69	68.5	68.5	89	66.5	66.5
30	33 2	3.4	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38932
R;Larrick, J.W.; Hirata, M.; Balint, R.F.; Lee, J.; Zhong, J.; Wright, S.C.
Infect. Immun. 63, 1291-1292, 1995
A;Title: Human CAPI8: a novel antimicrobial lipopolysaccharide-binding protein.
A;Reference number: I38932; MUID:95197251; PMID:7890387
CAP18 precursor - human
```

A;Accession: 138932
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
A;Residues: 1-170 <RES>

A;Cross-references: UNIPROT:P49913; UNIPARC:UPI000000A67; EMBL:U19970; NID:g643476; PID C;Superfamily: cathelin; cystatin homology C;Superfamily: cystatin homology <CYS>

Gaps ö Length 170; 0, Indels 100.0%; Score 535; DB 2; 100.0%; Pred: No. 1.9e-50; tive 0; Mismatches 0; Query Match Best Local Similarity 100.0 Matches 101; Conservative

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8 90 31 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDERPFYMDGDPDTPKPVSFTVKETVCPRTT **OVLSYKEAVLRAIDGINORSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT** н a ઠે

QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 131 용 ઠે

RESULT 2

Alternate names: antibacterial peptide FALL39
NyAlternate names: antibacterial peptide FALL39
NiAlternate names: antibacterial peptide FALL39
NiContains: antibacterial peptide LL-37; cathelin-related antibacterial peptide CAP-18
C;Species: Howo sapiens (man)
C;Species: P-Jan-1998 #sequence revision 06-Feb-1998 #text change 09-Jul-2004
C;Accession: S74248; S78211; \$66281; S66205; A55596; S49441; S58023
Figudmundsson, G.H.; Agerberth, B.; Odeberg, J.; Bergman, T.; Olsson, B.; Salcedo, R.
Fur. J. Biochem. 238, 325-332, 1996
A;Title: The human gene FALL39 and processing of the cathelin precursor to the antibacte A;Reference number: S74248; MUID:96283824; PMID:8681941

A;Accession: S74248 A;Molecule type: DNA A;Residues: 1-170 <GUD>

A; Cross-references: UNIPROT: P49913; UNIPARC: UP1000017636C; EMBL: X96735

A;Accession: S78211

A;Molecule type: protein A;Remiduem: 134-143 < GOURS-ZCOBS-references: UNIPARC:UPI000017636D R;Cowland, J.B.; Johnsen, A.H.; Borregaard, N.

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antibacterial peptide precursor - pig
C;Species: Sus acrofa domestica (domestic pig)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C;Accession: A53421
R;Zanetti, M.; Storici, P.; Tossi, A.; Scocchi, M.; Gennaro, R.
Biol. Chem. 269, 7855-7858, 1994
A;Title: Molecular cloning and chemical synthesis of a novel antibacterial peptide deriv
A;Reference number: A53421; MUID:94179144; PMID:8132502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Romeo, D.; Skerlavaj, B.; Bolognesi, M.; Gennaro, R.
J. Biol. Chem. 263, 9573-9575, 1988
A;Title: Structure and bactericidal activity of an antibiotic dodecapeptide purified fro.
A;Reference number: A33799; MUID:88257074; PMID:3290210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P49930; UNIPARC:UP1000012P425; GB:L26053; NID:9468911; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l, Residues: 1-155 <STO>
\, Cross-references: UNIPROT: P222226; UNIPARC: UPI0000049485; GB:L08834; NID: 9162599; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: cDNA sequence analysis of an antibiotic dodecapeptide from neutrophils A;Reference number: S27018; MUID:93093170; PMID:1459251
30 QVLSYREAVLRAVDQLNEQSSEPNIYRLLELDQPPQDDEDPDSPKRVSFRVKETVCPRTT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bactenecin precursor - bovine
NiAlternate names antibiotic dodecapeptide
CiSpecies: Bos primigenius taurus (cattle)
CiSpacies: Bos primigenius taurus (cattle)
CiSpaces 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
CiAccession: S27018; A33799
FERStorici, P.; del Sal, G.; Schneider, C.; Zanetti, M.
FEBS Lett. 314, 187-190, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 QALSYRRAVLRAVDRLNEQSSRANLYRLLELDQPPKADBDPGTPKPVSFTVKETVCPRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVLSYKRAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1-29/Domain: signal sequence #status predicted <SIG>F;2-129/Domain: cystatin homology <CYS>F;30-149/Domain: propeptide #status predicted <PRO>F;10-145/Product: bactenecin #status experimental <MA?
                                                                                                                     61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.5%; Score 361; DB 2;
Best Local Similarity 68.0%; Pred. No. 1.1e-31;
Matches 66; Conservative 17; Mismatches 14;
                                                                                 61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:144-155/Product: bactenecin #status experimen
F:146-154/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: cathelin; cystatin homology C;Keywords: antibacterial P;22-129/Domain: cystatin homology <CYS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Superfamily: cathelin; cystatin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 144-155 <ROM>
A;Cross-references: UNIPARC:UP1000003532B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: neutrophils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-153 <ZAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A53421
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,Accession: S27018
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                                                                                                                                                                                                                                                                                                    A Molecule type: protein

A Molecule type: protein

A Molecule type: protein

A Molecule type: 12.43,58-65,7%,67-85,7%,87-96,7%,98-100;110-112,7T,114-152 <COF>
A; Residues: 42-49,50-57,58-65,7%,67-85,7%,1015-86,7%,98-100;110-112,7T,114-152 <COF>
A; Residues: 42-49,50-57,58-65,7%,101000017636F; UNIPARC:UPI0000176370;

B; Agerberth, B.; Gunne, H.; Odeberg, J.; Rogner, P.; Boman, H.G.; Gudmundsson, G.H.

Broc. Natl. Acad. Sci. U.S.A. 92, 195-199, 1995

A; Title: FALL-39, a putative human peptide antibiotic, is cysteine-free and expressed in A; Reference number: A55596; MUID:95116523; PMID:7529412
                           A;Title: hCAP-18, a cathelin/pro-bactenecin-like protein of human neutrophil specific gr
A;Reference number: S66205; MUID:95339969; PMID:7615076
A;Accession: S66281
                                                                                                                                                    A;Molecule type; mRNA
A;Residues: 1-11,'T',114-170 <COW>
A;Cross-references: UNIPARC:UPI0000000A67; EMBL:X89658; NID:g902627; PIDN:CAA61805.1; PI
A;Accession: S66205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-5,'N',7-112,'T',114-170 <AGE>
A;Cross-references: UNIPARC:UP10000000841; EMBL:Z38026; NID:g558378; PIDN:CAA86115.1; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Map position: 3
A;Introns: 67/3; 103/3; 127/3
C;Keywords: antibacterial; blocked amino end; pyroglutamic acid
E;1-30/Domain: signal sequence #status predicted <SIW>
F;22-130/Domain: cystatin homology <CYS>
F;31-130/Product: cathelin-related antibacterial peptide CAP-18 #status predicted <MATI>F;31-133/Domain: propeptide #status predicted <PRO>
F;31-137/Product: antibacterial peptide LL-37 #status experimental <MAT>
F;31/Modifled site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Accession: 568229
A.Status: preliminary
A.Accession: brollminary
A.Status: preliminary
A.Status: preliminary
A.Rosidues: 1-155 cBAG>
A.Cross-references: UNIPROT:P54230; UNIPARC:UPI0000126859; EMBL:L46853; NID:g1161246; IC.Superfamily: cathelin; cystatin homology
F):1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;29-143/Domain: propeptide #status predicted <PRO>
F;29-143/Domain: propeptide #status predicted <AMA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVLSYKEAVLRAIDGINQRSSDANLYRLLDDDPRPTWDGDPDTPKPVSPTVKETVCPRTT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antimicrobial peptide precursor - sheep
NiAlternate names: procyclic dodecapeptide homolog
CiSpecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
CiDate: 15-Peb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
CiAccession: 56822
R:Bagella, L: Scocchi, M: Zanetti, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: cDNA sequences of three sheep myeloid cathelicidins A;Reference number: $68228; MUID:96105386; PMID:7498547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQSPEDCDFKKDGLVKRCMGTVNLNQARGSFDISCDKDNKR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSPDISCDKDNKR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.1%; Score 530; DB 2; 99.0%; Pred. No. 6.6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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       Lett. 368, 173-176, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Best Local Similarity
Matches 67; Conserva
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유 ઠે 셤 66.2%; Score 354; DB 2; Length 155;

Query Match

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A; Molecule type: mRNA
A; Residues: 1-212 <STR>
A; Residues: 1-212 <STR>
A; Cross-rences: 1-212 <STR>
A; Cross-rences: UNIPROT: PS1524; UNIPARC: UPI0000131712; GB: X86031; NID: g1006756; PIDN
B; Harwig, S.S.L.; Kokryakov, V.N.; Swiderek, K.M.; Aleshina, G.M.; Zhao, C.; Lehrer, R.I
FEBS Lett. 362, 65-69, 1995
A; Title: Prophenin-1, an exceptionally proline-rich antimicrobial peptide from porcine 1
A; Reference number: S68726; MUID: 95212585; PMID: 7688355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protegrin 2 precursor - pig
NiAlternate names: cathelin-like protein precursor; neutrophil peptide 3
Cispecies: Sus acrofa domestica (domestic pig)
Cipacies: Sus acrofa domestica (domestic pig)
Cipacies: 19-May-1994 #sequence revision 19-May-1994 #text_change 09-Jul-2004
CiAccession: JN0900; 836822; 534586
Ristorici, P.; Zanetti, M.
Biochem. Blophys: Res. Commun. 196, 1363-1368, 1993
A;Title: A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a cat A;Reference number: JN0900; MUID:94071898; PMID:8250892
A;Accession: JN0900.
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A;Residues: 1-147 <STO>
KCrose-references: UNIPROT:P32195; UNIPARC:UP10000131776; GB:L24745; NID:g431435; PIDN:
R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence A;Reference number: S36820; MUID:93387466; PMID:8375505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, B.A.; Shevchenko, A.A.; Aleshina, G.M.; Sh
FEBS Lett. 327, 231-236, 1993
                                                                                                                                                                                                                                                                                                                                                 NiAlternate names: antimicrobial peptide; prophenin-1
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 27-06-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 QALSYREAVLRAVDRLNEQSSEANLYRLLELDQPPKADEDPGTPKPVSFTVKETVCPRPT
30 QALSYREAVLRAVDRINEQSSEANLYRLILELDQPPKADEDPGTPKPVSFTVKETVCPRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKBTVCPRTT
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                                                                                                                                                                                                                                                                                                                           cathelin-like antibacterial peptide precursor (clone C6) - pig (fragment)
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                                                                                61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Experimental source: leukocytes
C, Superfamily: cathelin; cystatin homology
C, Keywords: antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 131-209 <HAR>
A;Cross-references: UNIPARC:UP1000014595E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 131-146 <MIR>
A;Cross-references: UNIPARC:UP1000014310F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P,6-113/Domain: cystatin homology <CYS>
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nes 65; Conserv
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Best Local S:
Matches 65
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R; Storici, P.; Zanetti, M.
Biochem. Biophys. Res Commun. 196, 1058-1065, 1993
Biochem. Biophys. Res Commun. 196, 1058-1065, 1993
A; Title: A CDNA derived from pig bone marrow cells predicts a sequence identical to the A; Reference number: JN0899; MUID:94071853; PMID:8250863
A; Molecule type: mRNA
A; Residues: 1-20, 'A', 22-172 <STO>
A; Molecule type: mRNA
A; Residues: 1-20, 'A', 22-172 <STO>
A; Cross-references: UNIPARC: UPT000016C687; GB:L23825; NID:G435100; PIDN:AA31109.1; PID: A; Cross-references: UNIPARC: UPT000016C687; GB:L23825; NID:G435100; PIDN:AA31109.1; PID: A; Cross-references: UNIPARC: NP. 92, 7085-7089, 1995
A; Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fam A; Reference number: 147138; MUID:95350216; PMID:7624374
A; Accession: 147138
A; Accession: 147138
A; Residues: 1-28, 'T', 30-89, 'QR', 92-116, 'NDP', 120-172 <GUD>
A; Cross-references: UNIPARC: UP1000016C6AC; EMBL:X87236; NID:G829142; PIDN:CAA60682.1; PI R; Access-references: UNIPARC: UP1000016C6AC; EMBL:X87236; NID:G829142; PIDN:CAA60682.1; PI R; Access-references: UNIPARC: UP100016C6AC; EMBL:X87236; NID:GRAFUE, W.; Boman, H.G.; Mutt, V.; Joernvall EUT. J. Biochem. 202, 849-854, 1991
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A/Introns: 66/3; 126/3
A/Introns: 66/3; 102/3; 126/3
A/Introns: 66/3; 102/3; 126/3
A/Introns: 66/3; 102/3; 126/3
C/Superfamily: cathelin; cystatin homology
C/Superfamily: cathelin; cystatin homology
P/1-29/Domain: signal sequence #status predicted <SIG>P/2-129/Domain: cystatin homology <CYS>
P/30-129/Domain: propeptide #status predicted <PRO>P/31-169/Product: antimicrobial protein PR-39 #status experimental <MAT>
P/109/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: propher A;Reference number: S68232; MUID:96105365; PMID:7498526
A;Accession: S68232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-172 <ZHA>
A;Cross-references: UNIPROT:P80054; UNIPARC:UPI000013215A; EMBL:X89201; NID:g1165150; PI
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                                                                                                                                                      QALSYREAVLRAVDQLNEQSSEPNIYRLLELDQPPQDDEDPDSPRRVSFRVKETVCSRTT 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                S68232
antimicrobial protein PR-39 precursor, cathelin-associated - pig
N/Alternate names: myeloid antibacterial protein PR-39
N/Alternate names: myeloid antibacterial protein PR-39
C.Species: Sus scrofa domestica (domestica pig)
C.Jate: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C.Accession: S68232, JN0899; T47138; S19563
R/Zhao, C.; Ganz, T.; Lehrer, R.I.
R/Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 376, 130-134, 1995
                                                                                                                 1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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       67.7%; Pred. No. 6.4e-31;
ive 16; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                              QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCD 96
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A;Residues: 131-169 «AGE»
A;Cross-references: UNIPARC:UP100002D613
A;Experimental source: intestine
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                                            65; Conservative
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Best Local Similarity
       Similarity
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       Best Local
Matches 6
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F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
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A; Molecule type: DNA
A; Residues: L-149 < ZH3-
A; Residues: S45712; MUID: 94283613; PMID: 8013647
A; Accession: A53895
A; Residues: L-149 < ZHA-
A; MIPARC: UPI0000131777; GB: X83267; NID: 9603037; PIDN: CAA58240.1; PID: R; Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, B.A.; Shevchenko, A.A.; Aleshina, G.M.; Sherence number: S34585; MUID: 93327946; PMID: 835113
A; Residues: 131-148 < KOK>
A; Residues: UNIPARC: UPI0000143110
A; Residues: UNIPARC: UPI0000143110
A; Residues: UNIPARC: UPIO000143110
B; Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, REBS Lett. 330, 339-342, 1993
A; Rivingorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, REBS Lett. 330, 339-342, 1993
A; FBS Lett. 330, 339-342, 1993
A; Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost A, Reference number: S34585; MUD:9337946; PMID:8335113
A, Accession: S34586
A, Molecule type: protein
A, Residues: 131-146 - KOK.
A, Cross-references: UNIPARC:UPI000014310F
C, Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism C; Superfamily: cathelin; cystatin homology
C, Keywords: amidated carboxyl end; antibacterial; neutrophil
F; 1-29/Domain: signal sequence #status predicted <SIG>F; 1-29/Domain: cystatin homology <CYS-F; 1-29/Domain: cystatin homology <CYS-F; 1-20-1-146/Product: protegrin 2 #status experimental <MAT>F; 1-146/Product: protegrin 2 #status experimental completed site: amidated carboxyl end (Val) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aritle: Primary structure of three cationic peptides from porcine neutrophils. Sequence A; Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence A; Reference number: 836820; MUID:93387466; PMID:8375505
A; Accession: 836821
A; Molecule type: protein
A; Residues: 131-148 < MIR>
Cross-references: UNIPARC:UP10000143110
C; Genetics:
A; Gene: NPG3
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NiAlternate names: neutrophil peptide 2
NiAlternate names: neutrophil peptide 2
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 01-bec-1995 #sequence revision 01-bec-1995 #text_change 09-Jul-2004
C;Accession: S66285; A53895; S34897; S36821; S57608
R;Zhao, C; Ganz, T; Lehrer, R.I.
FBBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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C;Suporfamily: cathelin; cystatin homology
C;Reywords: amidated carboxyl end; antibacterial; neutrophil
P;1-29/Domain: signal sequence #status predicted <SIG>
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Best Local Similarity
Matches 64; Conserva
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F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 3 #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-149 <ZHA>
A;Cross-references: UNIPROT:P32194; UNIPARC:UPI0000131775; EMBL:X84094; NID:g887642; PID:
R;Zhao, C.; Liu, L.; Lehrer, R.I.
R;Zhao, C.; Liu, L.; Lehrer, R.I.
A;Title: 146, 285-289, 1994
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Reference number: S45712; MUID:94283613; PMID:8013647
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A;Residues: 1-149 <ZH2.
A;Cross-references: UNIPARC:UDI0000131775; GB:X79868; NID:g603035; PIDN:CAA56251.1; PID::
R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
PEBS Lett. 330, 339-342, 1993
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A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost A;Reference number: S34585; WID:93327946; PMID:8335113
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C; Superfamily: cathelin; cystatin homology

C; Leybonds: amidated cathoxyl end; antibacterial; neutrophil

E;129/Domain: signal sequence #status predicted <SIG>

E;22-129/Domain: cystatin homology <CYS>

E;30-130/Domain: propeptide #status predicted <PRO>

E;1148/Product: protegrin 1 #status experimental <MMT>

E;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protegrin 1 precursor - pig
NyAleanate names: neutrophila peptide 1
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
Cispecies: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
Cispecies: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
Cispecies: 19-Oct-1995 #sequence_revision 03-Nov-1995
AlyTille: The structure of porcine protegrin genes.
AlyReference number: S66283; MUID:95354835; PMID:7628604
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                                                                                                                                                           DB 2; Length 149;
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                                                                                                                                                   Query Match

64.9%; Score 347; DB 2; Length 14

Best Local Similarity 66.0%; Pred. No. 3.5e-30;

Matches 64; Conservative 17; Mismatches 16; Indels
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Best Local Similarity 66.0%; Pred. No. 3.5e-
Matches 64; Conservative 17; Mismatches
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A;Residues: 131-148 <MIR>
A;Cross-references: UNIPARC:UP1000034C2E
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A;Residues: 131-148 <KOK>
A;Cross-references: UNIPARC:UP1000034C2B
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A;Cross-references: UNIPROT:P51525; UNIPARC:UDI0000131713; BMBL:X75438; NID:9443812; PID R;Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
A;Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte A;Reference number: S57330; MUD:96042752; PMID:7576250
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C.Species: Sus scrofa domestica (domestic pig)
C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C.Accession: 541731
F.Storici, P.; Socochi, M.; Tossi, A.; Gennaro, R.; Zanetti, M.
FEBS Lett. 337, 303-307, 1994
A;Title: Chemical synthesis and biological activity of a novel antibacterial peptide ded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen, Reference number: 868232; MUID:96105365; PMID:7498526
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                                                                                                                                                                                                                                                                                                                                                                                 prophenin (PF-2) precursor - pig
NiAlternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor NiAlternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor C;Species Sus scrofa domestica (domestic pig)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 840463; S57331; $68233
K;Pungercar, U; Strukelj, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, F.; Turk, FEBS Lett. 336, 284-288, 1993
A;Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial A;Reference number: $40463; MUID:94085623; PMID:8262247
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                                       QVLSYKEAVLRA I DGI NQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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64.7%; Score 346; DB 2; Length 228;
Best Local Similarity 63.4%; Pred. No. 7.1e-30;
Matches 64; Conservative 19; Mismatches 18; Indels
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8.1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-228/Product: prophenin (PF-2) #status predicted <MAT>
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A;Zhao, C.; Ganz, T.; Lehrer, R.I.
FBS Lett. 376, 130-134, 1995
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A;Molecule type: mRNA
A;Residues: 1-228 <STR>
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A;Molecule type: DNA
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A; Residues: 1-149 < CZHA.
A; Cross-references: UNIPROT: P49933; UNIPARC: UPI0000131778; GB: X83268; NID: g603039; PIDN: C; Superfamily: cathelin; Optatin homology
C; Superfamily: cathelin; Optatin homology
C; Keywords: amidated carboxyl end; antibacterial; neutrophil
P; 1-29/Domain: signal sequence #status predicted <SIG>
P; 1-29/Domain: cystatin homology <CXS>
F; 1-148/Pomain: cystatin homology <CXS>
F; 1-148/Pomain: protegrin 4 #status predicted <MAT>
F; 148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following g)
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A;Molecule type: DNA
A;Residues: 1-149 < ZZHA>
A;Residues: 1-149 < ZZHA>
A;Cross-references: UNIPROT: P49934; UNIPARC: UPI0000131779; EMBL: X84096; NID: 9887646; PIL
A;Experimental source: leukocytes
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F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 5 #status predicted <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
                                                                                                                                                                                                                                                                                    protegrin 4 precursor - pig
C;Species: Sus acrofa domestica (domestic pig)
C;Species: Sus acrofa domestica (domestic pig)
C;Accession: B53895
R;Zhao, C.; Liu, L.; Lehrer, R.I.
R;Zhao, C.; Liu, L.; Lehrer, R.I.
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Reference number: 845712; MUID:94283613; PMID:8013647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 60
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S57609
Nichternate names: cathelin-associated antimicrobial peptide
Nichternate names: cathelin-associated antimicrobial peptide
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: S66283; S57609
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 369, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                       GGenetics:
AjGenes NPG5
Ajfarcons: 66/3; 102/3; 126/3
Ajfarcons: 66/3; 102/3; 126/3
CSuperfamily: cathelin; cystatin homology
C; Keywords: amidated carboxyl end; antibacterial
C; Keywords: amidated sequence #status predicted <SIG>F;1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                      QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: not compared with conceptual translation A;Molecule type: mRNA
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Matches 64; Conserva
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Best Local Similarity
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A;Reference number: S41731; MUID:94123775; PMID:8293820
A;Accession: S41731
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-166 <STO>
A;Cross-references: UNIPROT:P49931; UNIPARC:UP1000012F428; GB:L29125; NID:9457347; PIDN:C;Superfamily: cathelin; cystatin homology
F;22-129/Domain: cystatin homology <CYS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        701171

18K lipopolysaccharide-binding protein precursor - rabbit
Nylternate names: 18K cationic protein
Nylternate names: 18K cationic protein
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: J01171; P80226
R;Larrick, J.W.; Morgan, J.G.; Palings, I.; Hirata, M.; Yen, M.H.
Biochem. Biophys. Res. Commun. 179, 170-175, 1991
A;Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding
A;Reference number: J01171; MUID:91354246; PMID:1883348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. Residues: 1-171 - LAR.

A. Residues: 1-171 - LAR.

A. Cross-references: UNIPARC:UPI0000145211

A. A. Cross-references: Done marrow

A. A. Cross-references: UNIPARC:UPI0000176372

A. Residues: 135-159, 'OIGQLL' - LAZ.

A. Residues: 157-Asp was also found

A. Note: 157-Asp was also found

C. Superfamily: cathelin; cystatin homology

F;1-29/Domain: signal sequence #status predicted <SIG.

F;30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT.
                                                                                                                                                                                                                                                                                                                                                                                                               1 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTHMDGDPDTPKPVSFTVKETVCPRTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                              30 QALSYRRAVLRAVDRLNEQSSEANLYRLLELDQPPKADEDPGTPKPVSFTVKETVCPRPT 89
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; Pred. No. 1.1e-29;
13; Mismatches 19; Indel8
                                                                                                                                                                                                                                                                                     64.3%; Score 344; DB 2; Length 166; 66.0%; Pred. No. 8.3e-30; Live 15; Mismatches 18; Indel8
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1 Similarity 67.0%;
65; Conservative 13
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Best Local Similarity 66.01
Matches 64; Conservative
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Best Local Similarity
Matches 65; Conserva
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1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 60

Search completed: January 12, 2006, 21:51:07 Job time : 8.94465 secs

61 OOSPEDCDFKKDGLVKRCMGTVTLNOARGSFDISCDK 97

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14 1+ RJ

GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

January 12, 2006, 21:42:24 ; Search time 49.1956 Seconds (without alignments) 1448.471 Million cell updates/sec Run on:

US-10-815-562-2_COPY_31_131
535
1 QVLSYKBAVLRAIDGINQRS......VTLNQARGSFDISCDKDNKR 101 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 Total number of hits satisfying chosen parameters: 2166443 segs, 705528306 residues Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P49913 homo sapien	Q71sn9 macaca mula	Q9glv5 macaca mula	O62841 equus cabal	O62842 equus cabal	P54230 ovis aries	O62840 equus cabal		P82018 capra hircu	P79362 ovis aries	Q4jfb9 capra hircu	P22226 bos taurus	P54229 bos taurus	P80054 sus scrofa	P51524 sus scrofa	P32195 Bus scrofa	P32194 sus scrofa	P32196 sus scrofa	P49933 sus scrofa	ene	P51525 sus scrofa	P49931 sus scrofa		P25230 oryctolagus	P49928 ovis aries	P49932 sus scrofa	P19660 bos taurus	P56425 bos taurus	P54228 bos taurus	Q9xsq8 capra hircu	P49929 ovis aries
SUMMAKIES		QI .	FAL39 HUMAN	FAL39 MACMU	Q9GLV5 MACMU	O62841_HORSE	O62842 HORSE	BCTN1 SHEEP	062840 HORSE	PMP23 PIG	BCTNS CAPHI	BCTN5_SHEEP	Q4JFB9 CAPHI	BCTN1 BOVIN	BMA28_BOVIN	PR39 PIG	PF11_PIG	PG2_FIG	PG1_PIG	PG3_PIG	PG4_PIG	PG5_PIG	PF12 PIG	PMP36_PIG	Q71KM5 RAT	CAP18_RABIT	SC51 SHEEP	PMP37 PIG	BCTNS_BOVIN	BMA34_BOVIN	BMA27_BOVIN	Q9XSQ8 CAPHI	SC52_SHEEP
		Length DB	170 1	170 1	170 2	157 2	170 2	155 1	156 2	153 1	176 1	176 1	176 2	155 1	159 1	172 1	212 1	147 1	149 1	149 1	149 1	149 1	228 1	166 1	171 2	171 1	160 1	167 1	176 1	165 1	158 1	158 2	160 1
	Query	Match	100.0	100.0	94.0	75.0	9.89	68.4	68.0	67.5	67.5	67.5	67.5	66.2	62.9	65.4	65.4	64.9	64.9	64.9	64.9	64.9	64.7	64.3	64.3	64.1	63.6	63.6	63.6	63.5	63.3	62.4	62.3
		Score	535	535	503	401	367	366	364	361	361	361	361	354	352.5	350	350	347	347	347	347	347	346	344	344	343	340.5	340	340	339.5	338.5	334	333.5
	Result	No.	-	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

P19661 bos taurus Q6tn20 canis famil P51437 mus musculu Q68318 bubbalus bub P13046 bos taurus P15175 sus scrofe P79361 ovis aries P79360 ovis aries P79360 ovis aries D80415 ovis aries D80415 ovis aries D80415 ovis aries Q19031 ovis aries Q19031 capra hircu Q19031 capra hircu Q19040 ovis aries Q191x12 cavia porce	update) no update) no update) no update) no update) no update no (FALL-39 peptide antiblotic) 18) (hCAP-18) (HSD26) (Contains: La; Vertebrata; Buteleostomi; rprimates; Catarrhini; Hominidae; ntiblotic, is cysteine-free and "; riblotic, is cyste	Bergman T., Olsson B.,
190 1 BCTN7 BOVIN 172 2 QGTN2Q CANFA 173 1 CRAMP MOUSE 144 2 QGB3RB BUBBU 144 2 QGB3RB BUBBU 164 2 P793G CAPHI 164 2 P793G CAPHI 165 2 QCTN7 GAPHI 190 1 BCTN7 GHEEP 190 1 BCTN7 GHEEP 190 2 QUSCOS CAPHI 165 2 QUSCOS CAPHI 165 2 QUSCOS CAPHI 165 2 QUSCOS CAPHI 166 2 QUSCOS CAPHI 167 2 QUSCOS CAPHI 168 2 QUSCOS CAPHI 168 2 QUSCOS CAPHI 169 2 QUSCOS CAPHI 169 2 QUSCOS CAPHI 169 2 QUSCOS CAPHI 160 2 QUSCOS CAPHI 160 2 QUSCOS CAPHI 161 2 QUSCOS CAPHI 162 2 QUSCOS CAPHI 163 2 QUSCOS CAPHI 164 2 QUSCOS CAPHI 165 2 QUSCOS CAPHI 165 2 QUSCOS CAPHI 166 2 QUSCOS CAPHI 167 2 QUSCOS CAPHI 168 2 QUSCOS	PRT; 170 ed) sequence upd sequence upd sequence upd annotation up 39 pracuisor tein CAP-189; PALL39; a, Craniata; htoglires; P AND SYNTHES; 29412; berg J., Kogn peptide antid d testide antid d testide antid antoglires; P AND PROTEIN (1995). C DNA]. ti X., Fran 1ysis and loc C DNA].	Agerberth B., Odeberg J., Be
32 333 62.2 34 323 62.1 35 324 62.1 37 61.1 37 60.6 37 324 60.6 37 318 59.4 41 318 59.4 41 303.5 59.1 44 299 55.9 45 280.5	1 AL39 HUMAN AL39 HUMAN AL39 HUMAN 1-007-193 3-SEP-206 ntibacte ntiba	Fubmed=8681941; Gudmundsson G.H., Ag Salcedo R.;
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                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477921; DOI-10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Alleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Alleschanko L., Marushia K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RABAS S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., Wckernan K.J., Malek J.A., Gunaratne P.H.,
RA Chards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Pahey J., Helton E., Kettemen M., Madan A., Kodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Sakalska U., Smailus D.E.,
R. Mederation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                              Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W., Korn B., Zuo D., Hu Y., LaBaer J.; "Cloning of human full open reading frames in Gateway (TM) system entry vector (pDONR201).";
"The human gene FALL19 and processing of the cathelin precursor to the antibacterial peptide LL-37 in granulocytes."; Bur. J. Biochem. 238:325-332(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibacterial activity.
SUBCELLULAR LOCATION: Secreted.
TISSUB SPECIFICITY: Expressed in bone marrow and testis and
                                                                                                                                             TISSUB-Testis;
Wu N., Miso S.Y., Zhang X.D., Qlao Y., Liang G., Wang L.F.;
"A new spermatogenesis-related gene.";
                                                                                      Gao Y., Huang Y.F., Xia X.Y.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                         Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: The N-terminus is blocked. SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z38026; CAA86115.1; -; mRNA.

X89569; CAA61805.1; -; mRNA.

U19970; AAA74094.1; -; mRNA.

U48795; AAC02634.1; -; Genomic_DNA.

X96735; -; NOT_ANNOTAYED_CDS; Genomic_DNA.

AY162210; AAN18318.1; -; mRNA.

AY251531; AAP20054.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ensembl; ENSG0000164047; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR541961; CAG46759.1; -; BC055089; AAH55089.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAG33364.1; -;
                                                                                                                                  NUCLEOTIDE SEQUENCE [MRNA].
                                                           NUCLEOTIDE SEQUENCE [MRNA].
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PIR; S74248; S74248.
                                                                         TISSUE-Epididymis;
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EMBL;
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EMBL;
EMBL;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCFRTT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
By similarity.
D -> N (in Ref. 1, 6, 7 and 8; CAG46759).
0 055807DCA95A7016 CRC64;
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NUCLECTIDE SEQUENCE [MENA], AND TISSUE SPECIFICITY.

NUCLENE-21137962; PubMed=11238224; DOI=10.1128/CDLI.8.2.370-375.2001;

MEDLINE-21137962; Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;

Bals R., Lang C., Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;

"Rhesus monkey (Macaca mulatta) mucosal antimicrobial peptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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10-MAY-2005 (Rel. 47, Last sequence update)
11-SEP-2005 (Rel. 47, Last sequence update)
11-SEP-2005 (Rel. 48, Last annotation update)
Antibacterial protein FALL-39 proternsor (FALL-39 peptide antibiotic)
(Cationic antimicrobial protein CAP-18) (rhCAP-18) (contains:
Antibacterial protein LL-37 (rhLL-37)].
Name-CAMP; Synonyms-CAP18, FALL39;
Macaca mulatta (Rhesus macaque).
Macaca mulatta (Rhesus macaque).
Macaca mulatta (Rhesus macaque).
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       close homologues of human molecules.";
Clin. Diagn. Lab. Immunol. 8:370-375(2001).
-!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                             Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                      Antibacterial protein FALL-
Antibacterial protein LL-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 QOSPEDCDFYCCGLVYRCCGTVTLNQARGSFDISCDKONKR 131
                                                                                                                                Probom; PRO01839; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Antibiotic; Antimicrobial; Direct protein sequencing; Pyrrolidone carboxylic acid; Signal.
1 30 Potential.
MIM; 600474; -. GO; GO:0042742; P:defense response to bacteria; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 535; DB 1
100.0%; Pred. No. 7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecidae; Cercopithecinae; Macaca. NOBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                             similarity)
                                                    InterPro; IPR001894; Cathelicidin.
PANTHER; PTHR10206; Cathelicidin; 1.
                                                                                                           Pfam; PF00666; Cathelicidins; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 AA; 19301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
                                                                                                                                                                                                                                                                                                                                                                                             31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                   132
134
31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULPID
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QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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MEDINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
Scocchi M. Bontempo D., Boscolo S., Tomasinsig L., Glulotto E.,
Zanetti M.;
                                                                                                                                                                                                                                                                                                                                                     TISSUE=Bone marrow;
MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Laurasiatheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OG2842_HORSE PRELIMINARY; PRT; 170 AA.

062842_
062842_
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Myeloid cathelicidin 3 precursor.
Name=eCATH-3;
Equus caballus (Horse).
Equus caballus (Horse).

Equus caballus (Horse).

Equus caballus (Horse).

Mammalla; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                               Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto B., Zanetti M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005576; C:extracellular region; IEA.
GO; GO:000552; P:defense response; IEA.
GO; GO:0009513; P:response to pset, pathogen or parasite; IEA.
InterPro; IPR001094; Cathellcidin.
ProDom: PF00666; Cathellcidins; 1.
ProDom: PF00666; Cathellcidins; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myeloid cathelicidin 2.
1424C493D2B307CC CRC64;
    91 QKSPEDCDFKEDGLVKRCVGTVILNQARDSFDISCDKDNRR 131
                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 401; DB 2; 77.3%; Pred. No. 1.3e-34; tive 10; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                            "Novel cachelicidins in horse leukocytes.";
FEBS Lett. 457:459-464 (1999).
EMBL. AJZ24928; CAA12227.1; -; mRNA.
HSSP, P32196; IKWI.
SMR; O62841; 30-130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Novel cathelicidins in horse leukocytes.";
                                                                                                157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential
                                                                                                PRT;
                                                                                                                                      Created)
                                                                                                                                                                                            Myeloid cathelicidin 2 precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18153 MW;
                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07,
                                                                                                O62841 HORSE PRELIMINARY;
O62841;
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157
                                                                                                                                                                                                                 Name=eCATH-2;
Equus caballus (Horse)
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157 AA;
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                                                                              062842
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                                                                                                                                                                                                                                                                                                                                                                                                                  31 QVLSYKRAVLRAIDGINQRSSDANLYRLLDLDPRPTWDGDPDTPKPVSFTVKETVCPRTT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 QVLSYQEAVLRAIDGINQRSSDANLYRLLDLDPRPTWDGDPDTPKPVSFTVKETVCPRTT 90
                                                                                                                                                                                                                                                                                                                                                                                         1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKBTVCPRTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOI=10.1128/AAC.45.10.2695-2702.2001;
Zhao C., Nguyen T., Boo L.M., Hong T., Espiritu C., Orlov D., Wang W.,
Waring A., Lehrer R.1.;
"RL-37, an alpha-helical antimicrobial peptide of the rhesus monkey.";
Antimicrob. Agents Chemother. 45:2695-2702(2001).
EMBL; AP189.954; AAG09440.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca mulatta (Rhesus macaque).

Bukaryota: Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
EMBL; AF288284; AAG40802.1; -; mRNA.
InterPro; IPR001894; Cathelicidin.
PANTHERS, PTHR10206; Cathelicidin; 1.
Pfam; PF00666; Cathelicidins; 1.
Probom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
SIGNAL 1 30 Potential.
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GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0006952; P:defense response; IEA.
GO; GO:0006913; P:response to pest, pathogen or parasite; IEA.
InterPro; IPR001894; Cathelicidin.
ProDom; PD001839; Cathelicidins; 1.
PROSITE; PS00946; CATHELICIDINS 1:
PROSITE; PS00947; CATHELICIDINS 2: 1.
SEQUENCE 170 AA; 18861 MM; 355AB3BF510DBB83 CRC64;
                                                                                                                                                                                          Antibacterial protein FALL-39.
Antibacterial protein LL-37.
Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                               100.0%; Score 535; DB 1; Length 170; 100.0%; Pred. No. 7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 503; DB 2; Length 170;
Pred. No. 1.8e-45;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 131
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                                                                                                                                                                                                                                                                         055B07DCA95A7D16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                       similarity
                                                                                                                                                                            Potential
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MEDLINE=21441139; PubMed=11557457;
                                                                                                                                                                                                                                                                           19301 MW;
                                                                                                                                                                                                                                                                                                                                   100.08;
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94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OGGLUS_MACMU PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 101; Conservative
                                                                                                                                                                          131
170
170
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                                                                                                                                                                                                                                                                         170 AA;
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Matches 94; Conserv
                                                                                                                                                                                                                                                                           SEQUENCE
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PIR; S68229; S68229.

HSSP, P32196; IKWI.

SMR; P54230; 30-130.

InterPro; IPR001894; Cathelicidin.

PANTHER; PTHR10206; Cathelicidin; 1.

Prom; PP00666; Cathelicidin; 1.

PROSITE; PS00946; CATHELICIDINS 1; 1.

PROSITE; PS00947; CATHELICIDINS 2; 1.

Anthiotic; Anthmicrobial; Pyrrolidone carboxylic acid; Signal.

SIGNAL.
EMBL; U60596; AAB49711.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.4%; Score 366;
                                                                                                                                                                                                                                                                                                                                                                                                           155 AA; 17648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.84;
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O62840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Conservative
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155
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124
154
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Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                               DISULPID
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MOD RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKBTVCPRTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-98121317; PubMed-9461419; DOI-10.1016/S0378-1119(97)00569-6; Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.; "Localization and genomic organization of sheep antimicrobial peptides
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96105386; PubMed=7498547; DOI=10.1016/0014-5793(95)01285-3; Bagella L., Scocchi M., Zanetti M.; "CDM sequences of three sheep myeloid cathelicidins."; PEBS Lett. 376:225-228(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ovis aries (Sheep).

Ovis aries (Sheep).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia;

Pecora, Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 206:85-91(1998).
-!- FUNCTION: Potent microbicidal activity, active against
Staphylococcus aureus and Escherichia coli (By similarity).
-!- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                               SMR; 062842; 30-130.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:000552; P:defense response; IEA.
GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
InterPro; IPR001894; Cathelicidin.
Pf00666; Cathelicidins; 1.
                                                                                                                                                                                                                                                                                                                                                               Match 68.6%; Score 367; DB 2; Length 170; Local Similarity 68.0%; Pred. No. 5.9e-31; les 68; Conservative 13; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                    myeloid cathelicidin 3. 5C35F1FA2D112BC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Cyclic dodecapeptide precursor (Bactenecin 1) (Bacl).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L46853; AAA85469.1; -; mRNA.
EMBL; U60595; AAB49710.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                  Potential.
                                                                                                                                                                                             ProDom, PD001838, Cathelicidin, 1.
PROSITE, PS00946, CATHELICIDINS 1, 1.
PROSITE, PS00947, CATHELICIDING 2, 1.
  FEBS Lett. 457:459-464(1999).
EMBL; AJ224929; CAA12228.1; -; mENA.
HSSP; P32196; 1KWI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                      170 m
19299 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=BAC1B; Synonyms=DODEB;
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                                                                                                                                                                                                                                                                                                    30 1
170 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996
                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                               Signal.
SIGNAL
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Matches
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Score 366; DB 1; Length 155; Pred. No. 6.8e-31;

1690638C791B1736 CRC64;

By similarity. By similarity. By similarity.

By similarity. Cyclic dodecapeptide. Pyrrolidone carboxylic acid (By similarity).

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89
                                                                             30 QVLSYREAVLRAVDQLNEQSSEPNIXRLLELDQPPQDDEDPDSPKRVSFRVKETVCPRTT
                                                  1 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Bone marrow;
MEDLINE=59402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E.,
  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Perissodactyla, Equidae, Equus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Movel cathelicidins in horse leukocytes.";

FEBS Lett. 457:459-464(1999).

R EMBL; AJ224827; CA12226.1; -; mRNA.

R MSP; P32196; 1KM1.

R MSP; P32196; 1KM1.

R GO; GO:0005576; C:extracellular region; IRA.

R GO; GO:0005513; P:response to pest, pathogen or parasite; IRA.

R InterPro; IPR001894; Cathelicidin.

R Pfam; PF00666; Cathelicidins; 1.

R PROSITE; PS00946; CATHELICIDINS.1; 1.

R PROSITE; PS00947; CATHELICIDINS.2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 156;
  13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential.
BB8EA5D150288FFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                   90 QQPPEQCDFKENGLLKRCEGTVTLDQVRGNFDITCN 125
                                                                                                                                                        61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 364; DB 2;
Pred. No. 1.1e-30;
                                                                                                                                                                                                                                                                                                                                         156 AA.
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myeloid cathelicidin 1 precursor.
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17647 MW;
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2.3e-30;

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Similarity
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107
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Best Local &
Matches 66
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SEQUENCE
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                                 Zhao C., Lehrer R.I.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: Exerts antimicrobial activity against both Gram-positive and negative bacteria at concentrations of 2-16 micro molar. Its activity appears to be mediated by its ability to damage bacterial
                                                                                                                                                                   01-OCT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Antibacterial peptide PMAP-23 precursor (Myeloid antibacterial peptide
                     1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
Gaps
                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                 TISSUE=Bone marrow;
MEDLINE=94179144; PubMed=8132502;
Banetti M., Storici P., Tossi A., Scocchi M., Gennaro R.;
"Molecular cloning and chemical synthesis of a novel antibacterial peptide derived from pig myeloid cells.";
J. Biol. Chem. 269:7855-7858(1994).
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SMR; P49930; 30-130.
InterPro; IPR001894; Cathelicidin.
PANTHER; PTR10206; Cathelicidin; 1.
ProDom; P000666; Cathelicidins; 1.
ProDom; P0001838; Cathelicidin; 1.
PROSITE; P800946; CATHELICIDINS 1; 1.
PROSITE; P800947; CATHELICIDINS 2; 1.
Antiblotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial peptide PMAP-23
Pyrrolidone carboxylic acid (N
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7ADAA22B6C206000 CRC64;
                                                                         QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the cathelicidin family.
20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE, AND SYNTHESIS OF 131-153
                                                                                                                                       153 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L26053; AAA31103.1; -; mRNA.
EMBL; Y16624; CAA76328.1; -; Genomic_DNA.
PIR; A53421; A53421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
13;
                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17486 MW;
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Conservative
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 AA;
                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                     rissum=Liver;
                                                                                                                                                                                                              Name=PMAP23;
                                                                                                                                      PIG
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                                                                                                                                 83
                                                                                                                30 QALSYREAVLRAVDRIANEQSSEANLYRILELDQPPRADEDPGTPKPVSFTVKETVCPRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVLSYKRAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKBTVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capra hirous (Goat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 131-149 AND 151-153, AND PROTEIN SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMR; P82018; 30-130.
InterPro; PR00189; Cathelicidin.
PANTHER; PTHR10206; Cathelicidin; 1.
Pfam; PP00666; Cathelicidin; 1.
ProDom; P001838; Cathelicidin; 1.
PROSTTE; P800947; CATHELICIDINS 1; 1.
PROSTTE; P800947; CATHELICIDINS 2; 1.
SMIGATION; Antibiotic; Antimicrobial; Direct protein sequencing; Pyrrolidone carboxylic acid; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proline amide (G-174 provides amide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Bone marrow, and Leukocyte;
MEDLINE=99346202; PubMed=10417180;
Shamova O., Brogden K.A., Zhao C., Nguyen T., Kokryakov V.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrrolidone carboxylic acid (By
                         14; Indels
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6PD7056C954B340A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PTM: Blastase is responsible for its maturation.
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Removed in mature form
                                                                                                                                                                                                                       61 OOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           176 AA
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By similarity.
68.0%; Pred. No. 2.3e
ive 17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
13-SEP-2005 (Rel. 48, Last annotation
Bactenecin 5 precursor (Bacs) (ChBacs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pecora; Bovidae; Caprinae; Capra.
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                            66; Conservative
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79 T -> R (in Ref. 1; AAB49716) 19842 MW; 05080026EA6FD5F7 CRC64;

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176 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=bac5;
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>B</u>CTN1 BO P22226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOVIN
                                                                                                          Matches
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Q4JFB9_CAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMML outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MBDLINE=98121317; PubMed=9461419; DOI=10.1016/S0378-1119(97)00569-6; Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.; "Localization and genomic organization of sheep antimicrobial peptides
                                                                                                                                  30 QALSYREAVLRAVGQLNERSSEANLYRLLELDPAPNDEVDPGTRKPVSFTVKETVCPRTT
                                                                                                            1 QVLSYKRAVLRAIDGINORSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- PTM: Blastase is responsible for its maturation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amidation; Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        James Bartos (Sheep).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes.";
Gene 206:85-91(1998).
-i- FUNCTION: Binds to the lipid A moiety of bacterial
-i- FUNCTION: Binds to the lipid A moiety of bacterial
membrane of all Gram-negative bacteria. Potent antimicrobial
activity (By similarity).
-i- DOMAIN: BACS sequence consists almost exclusively of X-P-P-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proline amide (G-174 provides amide
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                      Query Match 67.5%; Score 361; DB 1; Length 176; Best Local Similarity 68.0%; Pred. No. 2.7e-30; Matches 66; Conservative 17; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Removed in mature form.
                                                                                                                                                                                                                    90 QQPPEECDFKENGLVKQCVGTVTLDPSNDQFDINCNE 126
                                                                                                                                                                                           61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
                                                                                                                                                                                                                                                                                                                                                            P79362; P79363;
10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Bactenecin 5 precursor (Bac5) (OaBac5)
                                                                                                                                                                                                                                                                                                                                                 PRT; 176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity.
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EMBL; U60601; AAB49716.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE (GENOMIC DNA / MRNA)
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InterPro; IPR001894; Cathelicidin.
InterPro; IPR001894; Cathelicidin; 1.
PANTHER; PTHR10206; Cathelicidin; 1.
ProDom; PD001838; Cathelicidin; 1.
PROSITE; P800946; CATHELICIDINS_1; 1.
PROSITE; P800947; CATHELICIDINS_2; 1.
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174
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107
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                                                                                                                                                                                                                                                                                                                                                 SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=BAC5;
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                                                                                                              30 QALSYREAVLRAVGQLNERSSEANLYRLLELDPAPNDEVDPGTRKPVSFTVKETVCPRTT
                                                                                       1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Purification and properties of proline-rich antimicrobial peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Caprinae, Capra.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
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Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.5%; Score 361; DB 2; Length 17
68.0%; Pred. No. 2.7e-30;
ive 17; Mismatches 14; Indels
                                             14; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; Y18873; CAC80206.1; -; mRNA.
SEQUENCE 176 AA; 19846 MW; 6FD7056C954E340A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Bac1)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                              61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
; Score 361; DB 1;
; Pred. No. 2.7e-30;
17; Mismatches 14;
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01-OCT-1993 (Rel. 27, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Cyclic dodecapeptide precursor (Bactenecin 1)
                                                                                                                                                                                                                                                                                                                                       176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Bone marrow;
MEDLINE=99346202; PubMed=10417180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from sheep and goat leukocytes.";
Infect. Immun. 67:4106-4111(1999)
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    67.5%;
                         68.0%;
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Best Local Similarity 68.vv.
66; Conservative
                                             66; Conservative
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Q4JFB9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capra hircus (Goat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Bone marrow;
    Query Match
Best Local Similarity
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90 QQPPEQCDFKENGLLKRCEGTVTLDQVRGNFDITCN 125

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                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                              1 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                  MEDLINE=88257074; PubMed=3290210; Romeo D., Skerlavaj B., Bolognesi M., Gennaro R.; Schrlavaj B., Bolognesi M., Gennaro R.; Structure and bactericidal activity of an antibiotic dodecapeptide purified from bovine neutrophils."; J. Biol. Chem. 263:9573-9575 (1988).
                         IISSUE=Bone marrow;
MEDLINE=93093170; PubMed=1459251; DOI=10.1016/0014-5793(92)80971-I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                         Storici P., del Sal G., Schneider C., Zanetti M., "CDNA sequence analysis of an antibiotic dodecapeptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyclic dodecapeptide.
Pyrrolidone carboxylic acid.
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P32196; IKMI.

HSSP, P32196; IKMI.

INCEPTO: JPRO11894; Cathelicidin.

PANTHER; PTRE10206; Cathelicidin; 1.

PFODOM: P0010838; Cathelicidin; 1.

PROSITE; PS00946; CATHELICIDINS 1;

PROSITE; PS00947; CATHELICIDINS 2; 1.

Antiblotic; Antimicrobial; Direct protein sequencing; Pyrcolidone carboxylic acid; Signal.

SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Indels
                                                                                                       Scocchi M., Wang S., Zanetti M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q -> R.
008CD7DC6CB91BF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.2%; Score 354; DB 1; 67.7%; Pred. No. 1.3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     EMBL; L08834; AAA50615.1; -; mRNA.
EMBL; Y09472; CAA70617.1; -; Genomic_DNA.
PIR; S27018; S27018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17600 MW;
                                                                     FEBS Lett. 314:187-190(1992)
                                                                                                                                  PROTEIN SEQUENCE OF 144-155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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155
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                  NUCLEOTIDE SEQUENCE.
                                                                                      NUCLEOTIDE SEQUENCE.
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Les 65, Conserv
                                                                                                                                           TISSUE=Neutrophil;
                                                                                                                                                                                                        CHARACTERIZATION.
NCBI_TaxID=9913;
                                                                                                 TISSUE=Liver;
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MOD_RES
DISULPID
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SEQUENCE
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Matches
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61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCD 96

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                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
13.5EP-2005 (Rel. 48, Last annotation update)
Antibacterial peptide BWAP-28 precursor (Myeloid antibacterial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96300243; PubMed=8706679;
Storici P., Tossi A., Lenarcic B., Romeo D.;
Storici P., Tossi A., Lenarcic B., Romeo D.;
Storici P., Tossi A., Lenarcic B., Romeo D.;
precursors of antimicrobial peptides.";
Eur. J. Blochem. 238:769-776(1996).
-!- FUNCTION: Exerts a potent antimicrobial activity against Gramnegative and Gram-positive bacteria, including methicillin-resistant Staphylococcus aureus, and fungi.
-!- MASS SPECTROMERRY: MW-1414; MW-ERR=1; METHOD=Electrospray;
RANGE=30-159; NOTE=Ref:2.
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                                                                                                                                                                                                                                   Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Biological characterization of two novel cathelicidin-derived peptides and identification of structural requirements for their antimicrobial and cell lytic activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Bone marrow;
MEDLINE=97067059; PubMed=8910461; DOI=10.1074/jbc.271.45.28375;
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PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cathelicidin-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 65.9%; Score 352.5; DB 1; Length 159; Local Similarity 67.7%; Pred. No. 1.9e-29; Local Similarity 17; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skerlavaj B., Gennaro R., Bagella L., Merluzzi L., Risso A.,
Zanetti M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BMAP-28
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Pyrrolidone carboxylic acid.
By aimilarity.
By aimilarity.
898D7CB46CSERC367 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the cathelicidin family.
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                        159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION, AND MASS SPECTROMETRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 271:28375-28381(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X97609; CAA66208.1; -; mRNA.
HSSP; P32196; IKWI.
SWR; P54229; 30-131.
Interpro; IPR001894; Cathelicidin.
PANTHER; PTHR10206; Cathelicidin; 1.
Pfam; PF00666; Cathelicidin; 1.
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17616 MW;
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                        STANDARD;
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159 AA;
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172 AA;
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P51524;
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PF11_PIG
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30 QALSYREAVLRAVDQLNEKSSEANLYRLLELDPPPKEDDENPNIPKPVSFRVKETVCPRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Neutrophil;
WEDLINE-95088504; Pubmed=7996056;
WEDLINE-95088504; Chengappa M.M., Blecha F.;
Shi J., Rose C.R., Chengappa M.M., Blecha F.;
Identification of a proline-arginine-rich antibacterial peptide from neutrophils that is analogous to PR-39, an antibacterial peptide from the small intestine.";
Leukoc. Biol. 56:807-811(1994).
-!- FUNCTION: Exerts a potent antimicrobial activity against both
                                                                                                                                                                                                                                                                             MEDLINE=95350216; PubMed=7624374; Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M., Andersson L., Boman H.G.; Extraction of the gene for porcine peptide antibiotic PR-39, a cathelin gene family member: comparative mapping of the locus for the human peptide antibiotic PALL-39."; Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Amino acid sequence of PR-39. Isolation from plg intestine of a new member of the family of proline-arginine-rich antibacterial peptides.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUR=Liver;
MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;
Zhao C., Ganz T., Lehrer R.I.;
"Structures of genes for two cathelin-associated antimicrobial
peptides: prophenin-2 and PR-39.";
FEBS Lett. 376:130-134(1995).
                                                                                                                                                                                          namestroja (Pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                    Storici P., Zanetti M.; A conti M.; A cont detain a sequence "A cont derived from pig bone marrow cella predicts a sequence and derived in the first series and antibacterial peptide PR-39."; Blochem. Biophys. Res. Commun. 196:1058-1065(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Intestine;
MEDLINE=92111534; PubMed=1765098;
Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
Mutt V., Joernvall H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E.coli and B.megaterium.
--- TISSUE SPECIFICITY: Small intestine and bone marrow.
---- SIMILARITY: Belongs to the cathelicidin family.
                      P80054, Q9TR84, 01-MAR-1992 (Rel. 21, Created) 01-OT-1996 (Rel. 34, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Antibacterial protein PR-39 precursor.
                                                                                                            PRT; 172 AA
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                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Bone marrow;
MEDLINE=94071853; PubMed=8250863;
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                                                                                                            STANDARD;
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as long as its content is in no way modified and this statement is not
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MEDLINE=96042752; PubMed=7576250;
MEDLINE=96042752; PubMed=7576250;
Strukelj B., Pungercar J., Kopitar G., Renko M., Lenarcic B.,
Berbic S., Turk V.;
"Molecular cloning and identification of a novel porcine cathelin-like antibacterial peptide precursor.";
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MEDLINE=95212585; PubMed=7698355; DOI=10.1016/0014-5793(95)00210-2;
Harwig S.S.L., Kokryakov V.N., Swiderek K.M., Aleshina G.M., Zhao C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                             EMBL; X89235; CAA66682.1; -; Genomic_DNA.

REMBL; X89221; CAA66487.1; -; Genomic_DNA.

REMBL; X89221; CAA61487.1; -; Genomic_DNA.

REMBL; X89221; CAA61487.1; -; Genomic_DNA.

RESP; P32196; LW.

RESP; P32196; LW.

RESP; P32196; LW.

REPROPOSITE; PRO01694; Cathelicidin.

REPROSITE; PRO01694; Cathelicidin; 1.

REPROSITE; PS00946; CATHELICIDINS 1; 1.

REPROSITE; PS00947; CATHELICIDINS 1; 1.

REPROSITE; PS00947; CATHELICIDINS 2; 1.

REPROSITE; PS00947; CATHELICIDINS 2; 1.

REPROSITE; PS00947; CATHELICIDINS 2; 1.
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Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial protein PR-39.
Pyrrolidone carboxylic acid (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 ROPPELCDFKENGRVKQCVGTVTLNPSIHSLDISCNE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 OOSPEDCDFKKDGLVKRCMGTVTLNOARGSFDISCDK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 34, Last sequence update) (Rel. 48, Last annotation update) precursor (PF-1) (C6) (Fragment).
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Biol. Chem. Hoppe-Seyler 376:507-510(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrrolidone carboxylic acid; Signal
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01-0CT-1996 (Rel. 34, Last seq
13-SEP-2005 (Rel. 48, Last anno
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Matches 66; Conservative
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.ehrer R.I.; an exceptionally proline-rich antimicrobial peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QALSYREAVLRAVDRINEQSSEANLYRLLELDQPPKADEDPGTPKPVSFTVKETVCPRPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                            porcine leukocytes.";
FRBS Lett. 362-65-9(1995).
-!- FUNCTION: Exerts antimicrobial activity. It is more effective against Gram-negative bacteria than Gram-positive bacteria.
-!- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                      HSSP, P32196, 1LXE.

SRR, P51524; 14-110.
Interpro. 1PR001969, Cathelicidin.
PANTHER, PTH10206; Cathelicidin; 1.
Pfam; PF00666; Cathelicidins; 1.
PRODOM; PD001898; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrrolidone carboxylic acid (By similarity).
Proline amide (G-210 provides amide group) (Potential).
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                            Potential.
Prophenin-1.
Removed in mature form (Potential).
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PIR; S57330; S57330.
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Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

572060 seqs, 82675679 residues Searched:

572060 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

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Issued Patents AA:* Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	786	Sequence 2, Appli	7	m	33,	32	29,	34,	c	4	4,	4,	36,	40,	4	7	ý	ω`	2,	7	ý	æ	10,	'n	,	8	Sequence 4, Appli
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Score	:				367	364	354	352.5	347	347	347	347	347	347	347	347	347	347	347	347	347	347	347	347	347	347	343
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Sequence seq
US-09-322-911-4 US-09-917-340-36 US-09-917-340-36 US-09-917-340-28 US-08-313-681A-5 US-09-312-911-5 US-09-513-999C-4349 US-09-513-999C-4349 US-09-385-328-10 US-09-385-328-17 US-09-385-328-17 US-09-568-480-3 US-09-568-480-3 US-09-568-480-3 US-09-568-47-3 US-09-568-47-3 US-09-568-47-3
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ALIGNMENTS

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Sequence 7862, Application US/09513999C
; Sequence 7862, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dutas Milne Edwards, J.B.
; APPLICANT: Dutas Milne Edwards, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT APPLICATION NUMBER: US/09/513,999C
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT PILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US/00/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 QVLSYKRAVLRAIDGINQRSSDANLYRLLDLDPPRPTMDGDPDTPKPVSFTVKETVCPRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 535; DB 2; Length 152; Best Local Similarity 100.0%; Pred. No. 7e-60; Matches 101; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSPDISCDKDNKR 101
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TOTHER INFORMATION: SCORE 9.5

OTHER INFORMATION: SEQ LLLGLVMPLAIIA/QV
US-09-513-999C-7862
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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9 93

Sequence 2, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wight, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having

RESULT 2 US-08-313-681A-2

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US-09-917-340-32
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APPLICANT: Wright, Susan C.
APPLICANT: Hirate, Mishimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                             NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSPDISCDKDNKR 101
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                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Recentin Release #1.0, Version #1.25

SUSTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

REPLICATION NUMBER: US/08/313,681A

RESISTRATION: 435

ATTORNEY FAGENT INFORMATION:

NAME: Heslin, James M

REGISTRATION NUMBER: 29,541

REPERBOCKET NUMBER: 29,541

REPERBOCKET NUMBER: 15325-9-1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPAR: 415-326-2420

TELEPAR: 415-326-2420

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acids

TYPE: ADDITION INFORMATION:

TYPE: ADDITION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acids

TYPE: ADDITION INFORMATION:

TYPE: ADDITION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acids

TYPE: ADDITION INFORMATION:

TYPE: ADDITION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acids

TYPE: ADDITION INFORMATION:

TYPE: ADDITION INFORMATION:

TYPE: ADDITION INFORMATION:

TYPE: ADDITION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acids

TYPE: ADDITION INFORMATION:

TYPE: ADDIT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION NATR:
APPLICATION NUMBER: US/09/322,911
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Patent No. 6103888
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-313-681A-2
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 535; DB 2; Length 170;
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Batent No. 6696238

GENERAL INPORMATION:
APPLICANT: MUTAPLY, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR PELING DATE: 2000-07-29
PRIOR PELING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/220,602
PRIOR PELING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE PATENTING DATE: 2010-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE PATENTING DATE: 2010-05-15
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15325-000920
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/691,280
FILING DAYE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DAYE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DAYE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DAYE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DAYE: September 27, 1994
ATYONNEY/AGRNT INFORMATION:
REFERENCE/COCKET NUMBER: 35,136
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELEFPONE: 415-326-2402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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ORGANISM: Homo sapiens
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30 QALSYKGAVURAVDGLNQRSSDENLYRLLELDPLPKGDKDKDSDTPKPVSFWVKETVCPRIM 89
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                                                                                                                                                                                                                                                                                             1 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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                                                                                                                                        Query Match 68.0%; Score 364; DB 2; Length 156; Best Local Similarity 67.0%; Pred. No. 3.6e-38; Matches 67; Conservative 13; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENORGE 29, Application US/09917340
FRACEAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TILLE OF INVENTION: Transplant Media
FILE REPERENCE: TPLANT-06468
CURRENT FILING DATE: 2001-07-29
FRICH APPLICATION NUMBER: 60/249,602
FRICH FILING DATE: 2000-11-17
FRICH APPLICATION NUMBER: 60/249,602
FRICH FILING DATE: 2000-11-17
FRICH FILING DATE: 2001-05-15
FRICH FILING DATE: 2001-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OS-09-91/340-340-34, Application US/09917340
Patent No. 6696238
GERERAL INPORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TILLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT FILING DATE: 2001-07-29
FRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/29,602
PRIOR APPLICATION NUMBER: 60/299,602
PRIOR APPLICATION NUMBER: 60/299,602
PRIOR APPLICATION NUMBER: 60/299,602
; TYPE: PRT
; ORGANISM: Equus asinus
US-09-917-340-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Bos taurus
US-09-917-340-29
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                                                                                                                                                    31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 90
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                                                                                                              1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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                                         0; Indels
                                                                                                                                                                                                                                                              61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
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   Best Local Similarity 100.0%; Pred. No. 8.2e-60;
Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33, Application US/09917340
Fatent No. 6696238
GENERAL INPORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: Marphy, Christopher J.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
FRIOR FILING DATE: 2000-07-28
FRIOR FILING DATE: 2000-17-29
FRIOR FILING DATE: 2000-17-28
FRIOR FILING DATE: 2000-11-17
FRIOR FILING DATE: 2000-11-17
FRIOR FILING DATE: 2000-11-17
FRIOR FILING DATE: 2000-15-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PATENT VET. 170
SEQ ID NO 33
LENGTH: 170
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Fatent No. 669628
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
TILE OF INVENTION: Transplant Media FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION UNDERS: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR FILING DATE: 2000-07-29
FRIOR FILING DATE: 2000-07-29
FRIOR PILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
FRIOR FILING DATE: 2000-11-17
FRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARRE: PATENT VEY. 2.0
SOFTWARRE: PATENT VEY. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Equus caballus
US-09-917-340-33
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 65.9%; Score 352.5; DB 2; Length Best Local Similarity 67.7%; Pred. No. 1.1e-36; Matches 65; Conservative 17; Mismatches 13; Indels
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MEDIUM TYES: Floppy disk

MEDIUM TYES: Floppy
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; Sequent No. 5708145
; GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVUA S.L.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
; CORRESPONDENCES: 43
; CORRESPONDENCES: 44
; CORRESPONDENCES: 45
; CORRESPONDENCES
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PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 159
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MOLECULE TYPE: protein
US-08-243-879A-38
                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Bos taurus
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ZIP: 2006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Plopyy disk
COMPUTER: Plopyy disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-UUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H:
REGISTRATION NUMBER: 29,959
REFERRING-DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEFRAK: (202) 887-1500
TELEFRAK: (202) 887-1500
TELEFRAK: 90-4030
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MORALSON & FORESTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
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Best Local Similarity 66.0%; Pred. No. 4.7e-36;
Matches 64; Conservative 17; Mismatches 16;
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CORRESPONDENCE ADDRESS: ADDRESSES: PRINIE & EDMONDS LLP STREET: 1155 Avenue of the Americas CITY: New York STATE: New York STATE: New York
Sequence 4, Application US/08499523
Patent No. 5804558
GENERAL INPORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
ITILE OF INVENTION:
NUMBER OF SEQUENCES: 76
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LENGTH: 147 amino acids
TYPE: amino acid
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30 QALSYREAVLRAVDRLNEQSSEANLYRLLELDQPPKADEDPGTPKPVSFTVKETVCPRPT 89
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INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein

US-08-243-879A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
64.9%; Score 347; DB 2; Length 147;
Best Local Similarity 66.0%; Pred. No. 4.7e-36;
Matches 64; Conservative 17; Mismatches 16; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IS Floppy disk
SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIPICATION: 514
ATTORNEY FAGENT INFORMATION:
NAME: COTUZZI, Laura, A.
REGISTRATION NUMBER: 867-0054-999
TELERHONE: (212) 790-9090
TELERHONE: (212) 790-9090
TELERHONE: (212) 869-9741
TELERAK: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: AUG-141 ACIDE AUG-151
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APPLICANT: Chang, Chee L.
APPLICANT: Gu, Chee L.
APPLICANT: Steinberg, Deborah A.
APPLICANT: Steinberg, Deborah A.
APPLICANT: Lahrer, Robert I.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Rokryakon, Vladdmir N.
TILE OF INVENTION: PROTECRINS
FILE REFERENCE: 8067-0067-999
CURRENT APPLICATION NUMBER: US/99/385,328
CURRENT APPLICATION NUMBER: US 09/128,345
PRIOR APPLICATION NUMBER: US 09/128,345
PRIOR APPLICATION NUMBER: US 09/128,345
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 09/741,860
PRIOR FILING DATE: 1996-10-28
NUMBER OF SEQ ID NOS: 125
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; Sequence 4, Application US/09385328
; Patent No. 6653442
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ORGANISM: Sus scrofa
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64.9%; Score 347; DB 1; Length 149;
Best Local Similarity 66.0%; Pred. No. 4.8e-36;
Matches 64; Conservative 17; Mismatches 16; Indels
                                              RESULT 13
US-08-243-879A-36
i Sequence 36, Application US/08243879A
i Sequence 36, Application US/08243879A
i Patent No. 5708145
i GENERAL INFORMATION:
APPLICANT: HARWIG, SYLVIA S.L.
ADDRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FORRSTER
STERET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
COUNTY: USA
ZIP: 2000 Pennsylvania Ave. N.W., Ste. 5500
COUNTYR: USA
ZIP: 2000 Pennsylvania Ave. N.W., Ste. 5500
COUNTYR: BR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/243,879A
FILING DATE: NUMBER: US/08/243,879A
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGS, KATE, HS
REGISTRATION: S30
ATTORNEY/AGENT INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-243-879A-40

Sequence 40, Application US/08243879A

Sequence 40, Application US/08243879A

Patent No. 5708148

GENERAL INFORMATION:
APPLICANT: HARWIG, STIVIA S.L.
TILLE OF INVENTION: A NEW PROTEGRIN
INTER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: ADDRESSE:
ATREET: 2000 Pennsylvania Ave. N.W., Ste. 5500

CITY: Washington, DC
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90 RQPPELCDFKENGRVKQCVGTVTLDQIKDPLDITCNE 126
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SEQUENCE CHARACTERISTICS

Appli Appli

Run on:

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Sequence 51, Application US/10603566
| Publication No. US20040086966A1
| Publication No. US20040086966A1
| APPLICANT: Wittamer, Valerie
| APPLICANT: Vandenbogaerde, Ann | APPLICANT: Detheux, Wichel | APPLICANT: Parmentier, Warci | APPLICANT: Tarmentier, Warci | APPLICANT: Tarmen
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                                                                                                                                                                                                                                                                                                                        Sequence 51, P
Sequence 36, P
Sequence 28, A
Sequence 9, Ap
Sequence 28, A
Sequence 4, Ag
Sequence 4, Ag
Sequence 6, Ag
Sequence 8, Ag
Sequence 10, Ag
Sequence 2, Ag
Sequence 6, Ag
Sequence 10, Ag
Sequence 36, Ag
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US-09-539-443-10
US-10-627-829-2
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US-10-627-829-10
US-10-627-829-10
US-10-637-829-10
US-10-637-829-10
US-10-909-119-51
US-10-909-119-51
US-09-917-340-36
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US-09-917-340-36
US-09-917-340-36
US-09-917-340-38
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Patent No. US2002009369A1
GENERAL INPORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
TILE REFERENCE: TPLANT-06469
CURRENT APPLICATION UNDER: US/09/917,340
CURRENT APPLICATION NUMBER: 60/221,632
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR PLING DATE: 2000-01-17
PRIOR PLING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-917-340-32
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Sequence 32, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 32, Appl
Sequence 513, Appl
Sequence 513, Appl
Sequence 1204, Appl
Sequence 1204, Appl
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1 QVLSYKEAVLRAIDGINQRS.....VTLNQARGSFDISCDKDNKR 101
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Sequence 34,
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-603-566-51
US-10-344-709C-11
US-10-344-817-32
US-10-777-683-4
US-10-999-119-47
US-10-893-485-51
US-10-893-485-51
US-10-893-485-51
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US-10-893-485-51
US-10-893-4837-33
US-10-657-851-35
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US-10-844-837-29
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US-10-844-837-34
US-10-844-837-34
US-10-657-851-39
US-10-844-837-34
US-10-657-851-39
US-10-657-851-39
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Perfect score:
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Result

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Indels

Length 170;

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31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTWDGDPDTPKPVSFTVKETVCPRTT
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                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 535; DB 5;
100.0%; Pred. No. 1.2e-52;
tive 0; Mismatches 0;
                 APPLICANT: Homan, Jane
APPLICANT: Bremel, Robert D.
TITLE OF INVENTION: Targeted Biocides
FILE REFERENCE: IOGEN-09014
CURRENT APPLICATION NUMBER: US/10/844,837
CURRENT FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn version 3.2
SEQ ID NO ELENGTH: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/1077683 Publication No. US20050032117A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0
Matches 101, Conservative
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Matches 101; Conservative
APPLICANT: Imboden, Michael
                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Homo sapiens
US-10-844-837-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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Sequence 11, Application US/10344709C

Publication No. US20040170642A1

GENERAL INFORMATION:

TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathellicidin TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathellicidin TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathellicidin TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathellicidin TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathellicidin TITLE OF INVENTION NUMBER: US/10/344,709C

CURRENT PELING DATE: 2003-02-14

PRIOR PELING DATE: 2001-08-17

PRIOR PELING DATE: 2000-08-17

PRIOR PELING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 23

SEQ ID NO 11

LENGTH: 170

LENGTH: 170

LENGTH: 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-11
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100.0%; Score 535; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 535; DB 4;
100.0%; Pred. No. 1.2e-52;
tive 0; Mismatches 0;
               CURRENT APPLICATION NUMBER: US/10/603,566
CURRENT FILING DATE: 2003-06-25
PRIOR APPLICATION NUMBER: US 60/303,858
PRIOR FILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-23
NUMBER: OF SEQ ID NOS: 91
SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 101; Conservative
FILE REFERENCE: 9409/2212
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 US-10-603-566-51
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Sequence 47, Application US/10909119
Publication No. US20050079578A1
GENERAL INFORMATION:
APPLICANT: Centanni, John M.
APPLICANT: Allen-Hoffmann, Lynn
TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
FILE REFERENCE: STRATR-09123
CURRENT APPLICATION NUMBER: US/10/909,119
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APPLICANT: Richard B. Moss
APPLICANT: Richard B. Moss
APPLICANT: Akitoshi Ishizaka
APPLICANT: Teruo Kirikae
TITLE OF INVENTION: Method for Assessment of Cystic Lung Fibrosis
FILE REFERENCE: 074236
CURRENT APPLICATION NUMBER: US/10/777, 683
CURRENT FILING DATE: 2004-02-13
PRIOR PPLICATION NUMBER: US 60/447,310
PRIOR FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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US-10-844-837-32 ; Sequence 32, Application US/10844837 ; Publication No. US20050014932A1 ; GENERAL INFORMATION:

us-10-815-562-2_copy_31_131.rapbm

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SEQUENCE 32, Application US/10657851

Publication No. US20050089836A1

GENERAL INFORMATION:

APPLICANT: Wurphy, Christopher J.

APPLICANT: Reid, Ted W.

TILLE OF INVENTION: Transplant Media

FILE REFERENCE: TPLANT-06468

CURRENT APPLICATION NUMBER: US/10/657,851

CURRENT APPLICATION NUMBER: US/09/917,340

PRIOR PILING DATE: 2001-09-09

PRIOR PILING DATE: 2001-07-29

PRIOR PILING DATE: 2000-07-28

PRIOR PILING DATE: 2000-11-17

PRIOR PILING DATE: 2000-11-17

PRIOR PILING DATE: 2001-07-05

PRIOR PILING DATE: 2001-07-05

NUMBER: 06/290,932

NUMBER: OF SEQ ID NOS: 96

SEQ ID NO 32
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CURRENT FILING DATE: 2004-07-30 NUMBER OF SEQ ID NOS: 128 SOFTWARE: Patentin version 3.2 SEQ ID NO 47 LENGTH: 170
                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-909-119-47
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US-10-657-851-32
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TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR FILE REFERENCE: 9409/2045C
CURRENT APPLICATION NUMBER: US/10/893,485
CURRENT FILING DATE: 2004-07-16
PRIOR FILING DATE: 2004-07-09
PRIOR FILING DATE: 2003-06-25
PRIOR FILING DATE: 2003-06-25
PRIOR FILING DATE: 2003-06-25
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 97
SEQ ID NO 5: 97
LENGTH: 170
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Best Local Similarity 100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels
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Sequence 513, Application US/10287436A

Publication No. US20050202421A1

GENERAL INFORMATION:

APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER

TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: METHOD ARTHRITIS

TITLE OF INVENTION: METHOD ARTHRITIS

CURRENT APPLICATION NUMBER: US/10/287,436A

CURRENT FILING DATE: 2002-10-31

NUMBER OF SEQ ID NOS: 1446

SOFTWARE: PEASESE for Windows Version 4.0

SEQ ID NO 513

LENGTH: 170
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; Publication No. US2050202421A1
; GENERAL INCORMATION:
APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
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CRCANISM: Homo sapiens
US-10-287-436A-513
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US-10-893-485-51
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TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: RHEUMATOID ARTHRITIS FILE REFERENCE: 10872.514012 AND TREATMENT OF TILE REFERENCE: 10872.514012 AND TREATMENT OF THE REPRENCE: 10872.510.710 AND THE REPRENCE TO THE REPRENCE TO THE REPRENCE FILE TO THE REPRENCE FILE TO THE REPRENCE FOR SEQ ID NOS: 1446 SEQ ID NO 1204

LENGTH: 170
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100.0%; Pred. No. 1.2e-52;
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Fatent No. US20020090369A1
GERREAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
ITLE REPERENCE: TPLANT-0646B
CURRENT FILING DATE: 2001-07-29
CURRENT FILING DATE: 2000-07-28
FRIOR PILING DATE: 2000-07-28
FRIOR PILING DATE: 2000-11-17
PRIOR PELICATION NUMBER: 60/290,932
FRIOR PILING DATE: 2000-11-17
FRIOR PILING DATE: 2001-05-15
NUMBER: 07/290,932
NUMBER: 07/290,932
NUMBER: 07/290,932
NUMBER: 07/290,932
NUMBER: PLEING DATE: 2001-05-15
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US-09-917-340-33
                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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US-09-917-340-33
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sequence 33, Application US/10844837; Publication No. US20050014932A1; GENERAL INFORMATION: APPLICANT: Imboden, Michael

RESULT 12 US-10-844-837-33

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GENERAL INFORMATION:

APPLICANT: Centanni, John M.

APPLICANT: Allen-Hoffmann, Lynn
TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
FILE REFERENCE: STRATA-09123
CURRENT REPLICATION NUMBER: US/10/909,119
CURRENT FILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.2
SEQ ID NO 48
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APPLICANT: Homan, Jane
APPLICANT: Bremel, Robert D.
TITLE OF INVENTION: Targeted Biocides
FILE REFERENCE: IOGEN-09014
CURRENT APPLICATION NUMBER: US/10/844,837
CURRENT FILING DATE: 2004-05-13
NUMBER: OF SEQ ID NOS: 101
SEQ ID NO 33
LENGTH: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/10657851
| Publication No. US20050089836A1
| GENERAL INFORMATION:
| APPLICANT: Murphy, Christopher J.
| APPLICANT: McAnulty, Jonathan F.
| TITLE OF INVENTION: Transplant Media FILE REPERENCE: TPLANT-06468
| CURRENT FILIANT-06468
| CURRENT FILIANT-06468
| CURRENT FILIANT-06468
| PRIOR APPLICATION NUMBER: US/10/657,851
| PRIOR PRILING DATE: 2001-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-909-119-48
; Sequence 48, Application US/10909119
; Publication No. US20050079578A1
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 68.0%
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                         ; ORGANISM: Equus caballus
US-10-844-837-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Equus caballus
US-10-909-119-48
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US-10-657-851-33
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TYPE: PRT
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1 OVLSYKBAVLRAIDGINORSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 60
                                                                                                                                                                                                                                                                                    1 QVLSYKRAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 60
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                                                                                                                                                                                                                          Length 170;
                                                                                                                                                                                                                                                       19; Indels
                                                                                                                                                                                                                                                                                                                                              61 QQSPBDCDFKXDGLVKRCMGTVTLNQARGSFDISCDKDNK 100
:|:|| || || ||:|| || ||: || ||: || ||: ||
90 KQTPEQCDFKENGLVKQCVGTVILDPVKDYFDASCDEPQR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
LENGTH: 170
                                                                                                                                                                         ORGANISM: Equus caballus
US-10-657-851-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRGANISM: Equus asinus US-09-917-340-35
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                                                                                                                                                            TYPE: PRT
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Search completed: January 12, 2006, 21:54:02 Job time : 41.7417 secs

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January 12, 2006, 21:48:15; Search time 4.47232 Seconds (without alignments) 213.508 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
2: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
3: /cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
5: /cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
6: /cgn2 6/ptodata/1/pubpaa/USO1 NEW PUB.pep:*
7: /cgn2 6/ptodata/1/pubpaa/USO1 NEW PUB.pep:*
8: /cgn2 6/ptodata/1/pubpaa/USO1 NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Pred. No. 'is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 347, App Sequence 348, App Sequence 47, Appl Sequence 3750, Ap Sequence 68, Appl 7834, Ap 2964, Ap 878, App 876, App 43, Appl 39, Appl 1536, Ap 40, Appl 48, Appl 190, Appl Sequence 4 Sequence 1 Sequence 1 Sequence 5 Sequence US-11-000-463-348 US-11-147-041-47 US-11-147-041-47 US-11-055-822-68 US-10-667-295-42 US-11-100-181-15 US-10-17-295-42 US-11-137-465-35 US-11-137-465-35 US-11-137-465-35 US-11-137-465-36 US-10-995-561-876 US-10-995-561-876 US-10-995-561-879 US-10-995-561-879 US-10-995-561-879 US-10-995-561-879 US-10-995-561-879 US-11-135-855-879 US-11-135-855-879 US-11-135-855-879 US-11-135-855-879 US-11-135-855-40 US-11-174-150-48 US-10-055-877-190 SUMMARIES Length DB 997 1118 7294 7444 752 753 865 3446 408 Query Match Score Š. Result

22 DANLYRLLDLDPRPTMDGDPDTPKPVSFTVKBTVCPRTTQQSPBD-----CDFKKDGLVK 76

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26 55 10.3 1147 (B:10-612) 6665 6665 8 Sequence 5, Appli 28 545 10.2 529 7 189-11108-172-1068 Sequence 10.68 Appli 28 545 10.2 529 7 189-11108-172-1068 Sequence 10.68 Appli 28 545 10.2 510.2 529 7 189-111108-172-1055 Sequence 10.68 Appli 29 545 10.2 710 (B:10-612-24-905 Sequence 10.68 Appli 29 545 10.2 710 (B:10-612-24-905 Sequence 10.68 Appli 29 545 10.2 710 (B:10-612-24-905 Sequence 10.6 Appli 29 545 10.1 756 (B:10-055-917-189 Sequence 10.4 Appli 29 54 10.1 10.6 756 (B:10-055-917-189 Sequence 10.4 Appli 29 54 10.1 10.6 756 (B:10-055-917-189 Sequence 10.4 Appli 29 54 10.1 10.6 756 (B:10-055-917-189 Sequence 10.4 Appli 29 54 10.1 10.6 756 (B:10-055-917-189 Sequence 10.4 Appli 29 55 10.0 15.4 79 19-11-07-24-55 Sequence 10.4 Appli 29 55 10.0 15.4 79 19-11-07-24-55 Sequence 10.4 Appli 29 55 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 55 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 55 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 55 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 59 70 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 59 70 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence 10.4 Appli 29 7 10.0 15.4 79 19-11-07-24-5 Sequence
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CURRENT FILING DATE: 2005-06-07
CURRENT FILING DATE: 2005-06-07
PRIOR PILING DATE: 2005-06-07
PRIOR FILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-03-05
PRIOR PLING DATE: 2001-03-05
PRIOR PLING DATE: 2001-03-05
PRIOR PLING DATE: 2000-03-06
PRIOR PLING DATE: 2000-03-03
PRIOR PLING DATE: 2000-03-13
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-110-03
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ORGANISM: Homo sapiens
US-11-147-047-47
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    ---SGTIK----VKATQKKANDGEWYHVDIQRDGR-- 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chen, Kilandong B.
APPLICANT: Qian, Xiaohong B.
APPLICANT: Wehrman, Yaohong B.
APPLICANT: Wehrman, Tom
APPLICANT: Zhang, Zhiwei
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Cao, Yi-Cheng
APPLICANT: Cao, Yi-Cheng
APPLICANT: Cao, Yi-Cheng
APPLICANT: Dramanc, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE OF INVENTION: NOVER: 2004-11-29
FRICH REPERENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: 10/291,265
FRICH APPLICATION NUMBER: 10/991,265
FRICH APPLICATION NUMBER: 09/922,279
FRICH APPLICATION NUMBER: 09/922,279
FRICH APPLICATION NUMBER: 09/491,404
FRICH PRING DATE: 2000-07-17
FRICH APPLICATION NUMBER: 09/631,451
FRICH APPLICATION NUMBER: 09/631,451
FRICH APPLICATION NUMBER: 09/631,451
FRICH APPLICATION NUMBER: 09/631,451
FRICH PRING DATE: 2000-09-15
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Sequence 47, Application US/11147047;
Publication No. US20050260668A1;
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj;
APPLICANT: Murdock, Paul R.;
APPLICANT: Rizvi, Safia K.;
APPLICANT: Smith, Randall F.;
APPLICANT: Xiang, Zhaoying;
TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 --SGTISVNSRRTPFTASGESE 199
                                                                                                                                                      180 --SGTISVNSRRTPFTASGESE 199
                                                                                                                                                                                                                                                                                                                                             Sequence 348, Application US/11000463 Publication No. US20050266423A1 GENERAL INFORMATION:
                                                                             77 RCMGTVTLNQARGSFDISCDKD 98
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Best Local Similarity 26.8 Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
141 DGNLYLLLDMG-
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----MMRSVIGRQL 351
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                                                                                                           22 DANLYRLLDLDPRPTMDGDPDTPKPVSFTVKE----TVCPRTTQQSPEDCDFKKDGLVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Indels 19; Gaps
                                                         12;
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11.1%; Score 59.5; DB 6; Length 389;
Best Local Similarity 26.8%; Pred. No. 8.6;
Matches 22; Conservative 10; Mismatches 31; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3750, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INPOWARTON:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: FONTANA Maria Rita
; APPLICANT: FONTANA WASIGNALI VEGA
; APPLICANT: MASIGNALI VEGA
; APPLICANT: MASIGNALI VEGA
; APPLICANT: MONACI Elisabetta
; TITLE NOFINENTION: GONOCOCCAL PROTEINS AND NUCLBIC ACIDS
; TITLE REFERENCE:
; CURRENT FILING DATE: 2003-08-11
; FILE REPERENCE:
; CURRENT FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SEGWIN99, version 1.04
; SEQ ID NO 3750
LENGTH: 389
Query Match
11.2%; Score 60; DB 7; Length 349;
Best Local Similarity 28.4%; Pred. No. 6.5;
Matches 19; Conservative 6; Mismatches 30; Indels
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; OTHER INFORMATION: Ceres Seq. ID no. 6425770
US-10-667-295-43
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                                      Sequence 68, Application US/11055822
| Publication No. US20050260707A1
| GENERAL INFORMATION:
| APPLICANT: Pompelus, Markus
| APPLICANT: Pompelus, Markus
| APPLICANT: Schroder, Hartwig
| APPLICANT: Schroder, Marker, US/11/055,822
| CURRENT FILING DATE: 2000-06-21
| PRIOR PALING DATE: 1099-06-12
| PRIOR PALING DATE: 1999-06-12
| PRIOR PALING DATE: 1999-07-02
| PRIOR PAPLICATION NUMBER: 60/149,613
| PRIOR PLING DATE: 1999-07-01
| PRIOR PAPLICATION NUMBER: 06/187,970
| PRIOR PAPLICATION NUMBER: DE 19931418.7
| PRIOR PAPLICATION NUMBER: DE 19931418.7
| PRIOR PLING DATE: 1999-07-08
| PRIOR PAPLICATION NUMBER: DE 19931419.5
| PRIOR PLING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LSYKEAVLRAIDGINQR----SSDANLYRLLDLDPRPTMDGD----PDTPKPVSF 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-667-295-43

Sequence 43, Application US/10667295

Publication No. US20050257293A1

GENERAL INFORMATION:
APPLICANT: Mascia, Peter
ITILE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REPERENCE: 11586-047001

CURRENT APPLICATION NUMBER: US/10/667,295

CURRENT PILING DATE: 2003-09-17

PRIOR FILLING DATE: 2002-09-17

NUMBER OF SEQ ID NOS: 263

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59.5;
Pred. No. 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Corynebacterium glutamicum
US-11-055-822-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 11.1%;
1 Similarity 32.1%;
18; Conservative
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LOCATION: (1)...(102)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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US-11-100-183-15
US-11-100-183-15
US-11-100-183-15
Sequence 15, Application US/11100183
PUblication No. US20050272074A1
GENERAL INFORMATION:
APPLICANT: Stratagene California
TITLE OF INVENTION: Compositions And Methods For Reverse Transcription
CURRENT APPLICATION NUMBER: US/11/100,183
CURRENT FILING DATE: 2005-04-06
PRIOR APPLICATION NUMBER: US 6/559,810
PRIOR APPLICATION NUMBER: US 6/559,810
PRIOR PRIOR SEQ ID NOS: 61
SOTWARE: Patentin version 3.2
SEQ ID NO 15
ILENGINE OF 13-05
ILENGINE OF 1
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                                                                                                                                                                                                                                                                                        35 SVVGAVDGVB-----TNSNSEDK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPBDC 67
                                                                                                                                                                                                                      8 AVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDC
Query Match 10.8%; Score 58; DB 6; Length 102; Best Local Similarity 23.3%; Pred. No. 2.4; Matches 20; Conservative 10; Mismatches 24; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-667-295-42

Sequence 42, Application US/10667295

Publication No. US20050257293A1

GENERAL INPORMATION:
APPLICANT: MAGCIA, Peter

TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT FILING DATE: 2003-09-17

PRIOR FILING DATE: 2003-09-17

NUMBER OF SEQ ID NOS: 263

SOFTWARE: FASLSEQ for Windows Version 4.0

SEQ ID NO 4:

LENGTH: 141
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; OTHER INFORMATION: Ceres Seq. ID no. 6425769
US-10-667-295-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 DPKKDGLVKRCMGTVTLNQARGSFDI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                        68 DPKKDGLVKRCMGTVTLNQARGSPDI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 SEKDIKCKRIC VGSOALNYRRDHMEI 88
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; ORGANISM: Pasteurella multocida
US-11-100-183-15
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ORGANISM: Brassica napus
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Best Local Similarity
Matches 20; Conserv
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US-11-137-465-36
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                                                                                                                                                                                     LENGTH: 897
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                                                                                                                                                                                                               12 AIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFT----VKETVCPRTTQQSPE-- 65
                                                                                                                                                                                66 -----RGSPDIS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PLANG DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4258
SEQ ID NOS: 4472
SOFTWARE: PRECENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 NGVPQLINTSIINAFGLNDKNRGEEMSHYYDEQPDVKSNPKRISYQIKNAQLELTTDAGV 77
                                                 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
10.7%; Score 57; DB 6; Length 244;
Best Local Similarity 25.5%; Pred. No. 9.5;
Matches 24; Conservative 15; Mismatches 43; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Description of Artificial Sequence: synthetic ; OTHER INFORMATION: amino acid sequence US-10-793-626-566
10.7%; Score 57.5; DB 7; Length 236; 23.8%; Pred. No. 7.9; tive 14; Mismatches 38; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 -SPEDCDFKKDGLVKRCMGTVTLNQARGSFDISC 95
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CURRENT PILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/10/239,663
PRIOR FILING DATE: 2002-09-24
PRIOR PILING DATE: 2001-03-22
PRIOR PILING DATE: 2001-03-22
PRIOR PLING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/192,158
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APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia, K.
APPLICANT: Smith, Randall, F.
APPLICANT: Xiang, Zhaoying
APPLICANT: Xang, Zhaoying
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 566, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                            31; Conservative
                                                                                                                                                                                                                                                                          95 CDK---DNKR 101
                                                                                                                                                                                                                                                                                                                       143 CDRLGIDNSK 152
                     Best Local Similarity
Matches 31; Conserva
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 PVGFMLQP---DRKTCKDIDECRLNNGGCDHICRNTV-----GSFBCSCKKGYK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 PVSFTVKETVCPRTTQQSPEDCDPKKDGLVKRCMGTVTLNQARGSFDISCDKDNK 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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; Publication No. US20050260713A1
; GENERAL INFORMATION:
    APPLICANT: Gangolli et al.
    TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
    FILE REFERENCE: 21040-225
; CURRENT APPLICATION NUMBER: US/11/113,424
                                                                                                                                                                                                                                                                                                                                                                                    DB 7; Length 897;
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                                                                                                                                                                                                                                                                                                                                                                                    Score 56.5; DB 7; Length 8 Pred. No. 56; 6; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Murdoch, Paul R.
APPLICANT: Mixa'i, Safia, K.
APPLICANT: Smith, Randall, F.
APPLICANT: Smith, Randall, F.
APPLICANT: Stang, Zhaoying
APPLICANT: Xiang, Zhaoying
APPLICANT: Xiang, Zhaoying
APPLICANT: Xabnick, Karen
APPLICANT: Kabnick, Karen
APPLICANT: APPLICATION NUMBER: US/11/137,465
CURRENT APPLICATION NUMBER: US/10/239,63
FRIOR APPLICATION NUMBER: DC1-03-25
FRIOR APPLICATION NUMBER: PC7/US01/09226
FRIOR FILING DATE: 2001-03-27
FRIOR FILING DATE: 2000-03-24
FRIOR FILING DATE: 2000-03-24
FRIOR APPLICATION NUMBER: 60/192,158
FRIOR APPLICATION NUMBER: 60/192,168
FRIOR APPLICATION NUMBER: 60/192,168
FRIOR APPLICATION NUMBER: 60/192,168
FRIOR APPLICATION NUMBER: 60/192,168
FRIOR APPLICATION NUMBER: 60/192,166
FRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 60/200,166
PRIOR PILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
LENGTH: 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application US/11137465 Publication No. US20050255558A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.9%;
Matches 17; Conservative
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Best Local Similarity 30.9%
Matches 17; Conservative
                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-11-137-465-36
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Best Local Similarity 34.2
Matches 13; Conservative
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CORGANISM: Homo sapiens
US-10-995-561-878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-995-561-878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 PVSFTVKBTVCPRTTQQSPBDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 PTGFTLQ---VDGKTCKDIDECQTRNGGCNHFCKNTV-----GSFDCSCKKGFK 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.6%; Score 56.5; DB 7; Length 997; 30.9%; Pred. No. 64; tive 6; Mismatches 23; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 SSADLLRYYRIQTAP-MPSEPPEKTLEDPKNVSPCISGTNCP----APSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7834, Application US/10467657
; Sequence 7834, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: PIZZA Mariagrazia
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
; APPLICANT: MANIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OP INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT PILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; SOFTWARE: SeqWin99, version 1.04
; SOFTWARE: SeqWin99, version 1.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Score 56; DB 6; Length 118; 29.7%; Pred. No. 5; tive 7; Mismatches 18; Indels
CURRENT FILING DATE: 2005-04-21

PRIOR APPLICATION NUMBER: 60/256,704

PRIOR FILING DATE: 2000-12-19

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-10

PRIOR PLING DATE: 2000-12-20

PRIOR PLING DATE: 2000-10-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-29

PRIOR PLING DATE: 2001-08-29

PRIOR PLING DATE: 2001-07-24

PRIOR PLING DATE: 2001-07-24

PRIOR PLING DATE: 2001-07-24

PRIOR PLING DATE: 2001-09-14

PRIOR PLING DATE: 2001-09-14

PRIOR PLING DATE: 2001-05-29

PRIOR PLING DATE: 2001-05-30

PRIOR PLING DATE: 2001-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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US-10-467-657-7834
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ORGANISM:
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Sequence 878, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDICOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE REFERENCE: CLOOL559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQ ID NO 878
LENGTH: 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29
Sequence 2964, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION:
FILLE REPERENCE: 190486002
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 4472
SEQ ID NO 2964
LENGTH: 5024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3196 KEIIKQLTDAVNQANNDLNGVELLDADKQNAHQSIPTL 3233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 KEAVLRAIDGINQRSSDANLYRLLDLDPR-----PTM 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Score 56; DB 6; I 34.2%; Pred. No. 5.6e+02; tive 7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
10.4%; Score 55.5; DE
Best Local Similarity 23.5%; Pred. No. 57;
Matches 23; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: January 12, 2006, 21:54:25 Job time : 4.47232 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (5074)
; OTHER INFORMATION: variable amino acid
US-10-793-626-2964
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
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Page 1

4/2/03

5.1.6 Compugen Ltd. version = GenCore Copyright (c) 1993

protein search, using sw model ı OM protein

January 12, 2006, 21:41:48; Search time 90.3321 Seconds (without alignments) 826.886 Million cell updates/sec 9 Run

US-10-815-562-2 879 1 MKTQRDGHSLGRWSLVLLLL......KRIVQRIKDFLRNLVPRTES 170 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 2443163 segs, 439378781 residues Searched:

2443163

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003s:* geneseqp2004s:* A_Geneseq_21:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aab07901 A human c	Adf18219 Protein B	Adi29582 Human CAP	Adj82973 Human Pep		Adw43827 Mouse che	Adk70797 Human CAP	Aar92924 Prepro-FA	Aau90996 Transplan	Adp65263 Human cat	Adn41827 Human LL-	Abm80449 Tumour-as	Adx08374 Cathelici	Adz80363 Human cat		Aau31061 Novel hum	Aag03781 Human sec	Adj82974 Human Pep	Aea00315 Human cat		Abb07703 Rabbit pe	Aau90997 Transplan	Adx08375 Myeloid c	Aau90999 Transplan
SUMMARIES	Des	AAB07901 Aab	ADF18219 Adf	ADI29582 Adi	ADJ82973 Adj	ADR47315 Adr	ADW43827 Adw	ADK70797 Adk	AAR92924 Aar	AAU90996 Aau	ADP65263 Adp	ADN41827 Adn	ABM80449 Abm	ADX08374 Adx	ADZ80363 Adz	ABB07707 Abb	AAU31061 Aau	AAG03781 Aag	ADJ82974 Adj	AEA00315 Aea	ADZ80366 Adz	ABB07703 Abb	AAU90997 Aau	ADX 08375 Adx	AAU90999 Aau
-,		3 AAB	7 ADF.	8 ADI:	8 ADJ	8 ADR	9 ADW	B ADK	2 AAR	5 AAUS	7 ADP	8 ADN	B ABM	9 ADX	9 ADZ	5 ABB(4 AAU	3 AAG	8 ADJ	9 AEA	9 ADZ	5 ABB(5 AAUS	9 ADX(5 AAUS
	Query Match Length DB	170	170	170	170	170	170	169	170	170	170	170	170	170		170	177	152	140	170	172	171	170	170	156
	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	99.2	99.4	99.4	99.4	99.4	99.4	99.4	99.4	98.4	93.2	9.98	83.0	78.5	56.1	53.3	52.0	52.0	51.3
	Score	879	879	879	879	879	879	875	874	874	874	874	874	874	874	865	819	761	730	069	493.5	468.5	457.5	457.5	451
	Result No.	 	8	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Myeloid c	Goat cath	Human CRA	Transplan	BMAP-28 m	. Murine ca	Bovine pe	Transplan	Bacteneci				Antimicro	Antimicro	/ Antimicro	Antimicro	Pig prote	Pig prote		Pig prote	
Adx08377	Adz80368	Adz80365	Aau90998	Adx08376	Abb07701	Abb07704	Aau90993	Adx08371	Aaw18157	Adz80367	Aaw18158	A8w25081	Aaw18156	Aaw09087	Aaw18159	Ad118364	Ad118362	Ad118366	Ad118368	Abp70875
ADX08377	ADZ80368	ADZ80365	AAU90998	ADX08376	ABB07701	ABB07704	AAU90993	ADX08371	AAW18157	ADZ80367	AAW18158	AAW25081	AAW18156	AAW09087	AAW18159	ADL18364	ADL18362	ADL18366	ADL18368	ABP70875
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156	176	173	159	159	173	155	155	155	149	172	147	149	149	149	149	147	149	149	149	158
51.3	50.3	49.3	49.1	49.1	49.1	48.6	48.6	48.6	48.3	48.0	47.6	47.6	47.6	47.6	47.6	47.3	47.3	47.3	47.3	47.0
451	442.5	433.5	432	432	431.5	427.5	427.5	427.5	424.5	421.5	418.5	418.5	418.5	418.5	418.5	415.5	415.5	415.5	415.5	413
25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

Human; cationic protein; lipopolygaccharide binding; anticoagulant; CAP18; reactive nitrogen inhibitory protein; RNIP; gram negative sepsis; coagulation-related disorder; disseminated intravascular coagulation. A human cationic protein designated CAP18. AAB07901 standard; protein; 170 AA 14-NOV-2000 (first entry) AAB07901; AAB07901

Location/Qualifiers 134. .170 /note= "reactive nitrogen inhibitory protein" Homo sapiens Protein Key

92US-00916761. 92US-00916765. 93WO-US006731. 99US-00322911. 17-JUL-1992; 15-JUL-1993; 27-SEP-1994; 01-AUG-1996; 01-JUN-1999; US6103888-A. 17-JUL-1992; 15-AUG-2000

Hirata M; 94US-00313681, 96US-00691280 (PANO-) PANORAMA RES INC Larrick JW, Wright SC,

WPI; 2000-531989/48. N-PSDB; AAA59574. Novel human cDNA encoding cationic proteins having lipopolysaccharide binding and anticoagulant activity, useful for treating and diagnosing gram negative sepsis and disseminated intravascular coagulation.

Disclosure; Col 29-30; 46pp; English.

The present sequence represents a human cationic protein, having lipopolysaccharide binding and anticoagulant activity. The polypeptide is

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                                         aB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of a peptide LL-37 for the preparation of a composition for preventing or treating wounds or a disease caused reduced blood flow, e.g. atherosclerosis, coronary heart disease, stroke, arterial occlusive diseases or ulcer.
designated CAP18. Amino acide 134-170 of CAP18 represent a reactive nitrogen inhibitory protein (RNIP). The CAP18 polynucleotide is useful for producing cationic proteins. The CAP18 polypeptide is useful for treating and diagnosing lipopolysaccharide-associated conditions such gram negative sepsis, and/or coagulation-related disorders, such as disseminated intravascular coagulation
                                                                                                                                                                                      MKTQRDGHSLGRWSLVLLLLGLVWPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                 LDPRPTMDGDPDTPKPVSPTVKBTVCPRTTQQSPEDCDPKKDGLVKRCMGTVTLNQARGS
                                                                                                                                                                    1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial; LL-37; hCAP-18; antiarteriosclerotic; antiulcer;
                                                                                                                100.0%; Score 879; DB 3; Length 170; larity 100.0%; Pred. No. 4e-89; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Encoded by AAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Von Degenfeld G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                  ADF18219 standard; protein; 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2002; 2002EP-00004656
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vulnerary; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koczulla AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BALS/) BALS R.
(KOCZ/) KOCZULLA A R.
(VDEG/) VON DEGENFELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003-879818/82
                                                                                                                           Local Similarity
nes 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein sequence.
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                                                                                         Sequence 170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                          ADF18219;
                                                                                                                   Query Match
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                                                                                                                                           Matches
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The present invention is based on the finding that human antimicrobial peptide Li-37 APS18218 is capable of inducing functionally important anglogenesis in cell culture and in vivo by activation of the receptor molecule FPRL1. LL-37 can be used in the preparation of a pharmaceutical

Disclosure, Page, 15pp, English.

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                                                                                                                                                                                                                                                                                                                                                                                                LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
              resulting in, a reduced level of angiogenesis or arteriogenesis, or for the treatment of (infected) wounds or cancer. The disease may be associated with reduced blood flow, such as atherosclerosis, coronary heart disease, stroke, arterial occlusive disease or an ulcer. Suppression of angiogenesis through inhibition of IL-37 can be used to treat tumours, especially a carcinoma or sarcoma including cancer of the bile duct, brain, breast, colon, stomach, male and female reproductive organs, lung and airways, skin, gailbladder, liver, nasopharynx, nerve cells, kidney, prostate, and Kaposi's sarcoma (all claimed). The present
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 or
for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibody against an antibacterial peptide, particularly human CAP18, applicable in reagents and Monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                      LDPRPTWDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAP18; cationic antimicrobial protein of 18 kDa; bacterial pneumonia; chronic lung disease; acute lung disease; inflammatory lung disease; ARDS; bronchial asthma; human.
                                                                                                                                                                                                                                                                                                                                                 1 MKTQRDGHSLGRWSLVLLLLGLWPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                          1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                           Gaps
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composition for the prevention or treatment of a disease caused by,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDISCDKDNKKFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                 100.0%; Score 879; DB 7; Length 170; 100.0%; Pred. No. 4e-89; 1ve 0; Mismatches 0; Indels
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                                                                                                                                                                                protein sequence is not explained in the specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 4; 52pp; Japanese.
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                                                                                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 170; Conservative 0
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14-MAR-2003; 2003JP-00070932.
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                                                                                                                                                                                                                     Sequence 170 AA;
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of bacteria
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WPI; 2004-099371/10.
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diseases, ARDS and bronchial asthma. The present sequence is human
                                                                       1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD
                                                                                  MKTQRDGHSLGRWSLVLLLIGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
                                                        Gaps
                                                                                                                                                                                                                                                                 pep714-related peptide; precursor; human; secreted peptide; Pep714; oral mucositis; oral lesion; cystic fibrosis; respiratory infection;
                                                                                                                                        PDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
                                                                                                                                                PDISCONDINKRPALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
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                                        Score 879; DB 8; Length 170;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                /note= "dibasic peptidase cleavage site"
130. .131
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'note= "dibasic peptidase cleavage site"
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                                                                                                                                                                                                                                                                                                                                                                                                               label= antibacterial_protein_FALL-39
34. 170
label= antibacterial_protein_LL-37
                                                                                                                                                                                                                                                Human Pep714-related peptide precursor SEQ ID NO: 1.
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note= "dibasic peptidase cleavage
51. .152
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                                    100.0%; Score 8/2, _____100.0%; Pred. No. 4e-89; +ive 0; Mismatches (
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/label= signal_peptide
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/label= p
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Matches 170; Conservative
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Novel Pep714-related polypeptide having biological activity, useful for treatment and prevention of microbial or viral infection, cystic fibrosis and chronic respiratory infections.
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100.0%; Pred. No. 4e-89;
ive 0; Mismatches 0; Indele
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                                                                                                                                                     Disclosure; Page 91-92; 99pp; English
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Matches 170; Conservative
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Example 2; SEQ ID NO 51; 183pp; English.

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evaluating cystic pulmonary fibrosis by associating comparison of obtained results. The invention further comprises: a kit for carrying out the evaluating method, comprising a solid-phase component and an antibody coupled with an antigenic peptide having a sequence of ADRA7112, or a solid-phase component comprising an immobilised antibody (first antibody solid-phase component comprising an immobilised antibody (first antibody) useful for evaluating the antigenic peptide. The method or kit are useful for evaluating cystic pulmonary fibrosis in an individual, where the evaluation includes diagnosis for the presence or absence of a risk of cystic pulmonary fibrosis, evaluation of serious or acute conditions, or the evaluation of the advanced grade of the disease. The method enables simple, cost-effective, rapid, highly sensitive and highly accurate evaluation of the acute or serious conditions, or the advancement of the pulmonary diseases. This sequence represents the human advancement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAP18 protein of the invention.
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Sequence 170 AA;

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LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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               Score 879; DB 8; Length 170;
Pred. No. 4e-89;
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100.0%; Score
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              Query Match 100.
Best Local Similarity 100.
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Mouse chemerin peptide SEQ ID NO 51. ADW43827 standard; peptide; 170 AA (first entry) 24-MAR-2005

neurological disease; hyperproliferative disorders; cytostatic; chemerin. lymphoproliferative disease; dermatological disease; dermatological; hemostatic; inflammation; antiinflammatory; hematological disease; immune disorder; neoplasm; cardiovascular-gen.; cns-gen.; gene therapy; diagnosis; cell signaling; gene therapy;

Mus musculus

WO2005000875-A2. 06-JAN-2005. 25-JUN-2004; 2004WO-EP006945.

25-JUN-2003; 2003US-00603566.

(EURO-) EUROSCREEN SA.

Detheux M, Parmentier M, Loison C; Communi D, Wittamer V, Ooms FDR;

WPI; 2005-058121/06.

New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstron's Macroglobulinemia, Gaucher's Disease, or histiccytosis.

alpha-helix; thionine; antibacterial; antifungal; plant; fungi resistance; rice blast fungus; Ceratocystis fimbriata; bacteria; Pseudomonas; antimicrobial; rabbit; CAP18.

JP2003204794-A. Homo sapiens

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The invention describes a polypeptide (1) of up to 50 amino acids where the polypeptide binds specifically to a chemerink polypeptide. Also described are: a mucleic acid sequence encoding (1); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal transfected with the expression vector; a (therapeutic) composition comprising (1) and an isolated chemerink polypeptide or a nucleic acid sequence of (1); an antibody that selectively binds to (1); identifying an agent that modulates the interaction between a chemerin polypeptide and a gent that modulates the interaction between a chemerin polypeptide and a gent that modulates the interaction between a chemerink polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a Chemerink polypeptide is detecting the presence, in a sample, of an agent that modulates the function of Chemerink polypeptide; detecting the presence, in a sample, of an agent that modulates the function of Chemerink polypeptide is disorder characterized by dysregulation of Chemerink (polypeptide) signaling, a ktt, for screening agents that modulate the signaling activity of Chemerink polypeptide of signaling, a ktt, for screening agents that chemerink polypeptide signaling, a comprising an isolated chemerink polypeptide signaling, a comprising an isolated polymuclectide encoding (1), an isolated polymuclectide encoding (1), and its packaging creamediament for exvivo gene hersapy or for in vivo gene thersapy or a medicament for exvivo gene thersapy or for in vivo gene thersapy or a medicament for an invitro method of inhibiting call proliferation, where the medicament is creating a disease, and slocked or in vivo gene thersapy or composition, composition or expression vector is useful for activation; baraproceinemias, purpura, searcidess, Sezary Syndrome, Waldenstron's Macroglobulinamia, Gaucher's placese, in stelland in virtue disease, the polypeptides and polymer population are useful for diagnosing and executing the 
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ADK70797 standard; protein; 169 AA. Human CAP18 full-length protein. 06-MAY-2004 (first entry) RESULT 7 ADK70797

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Novel cathelin-like prepro-FALL-39 (AAR92924) is the precursor of the antimicrobial, antibacterial agent FALL-39 (see AAR92923). It is the product of a CDNA clone (AAT1823) isolated from a human bone marrow CDNA library. FALL-39 includes a helical region (see AAR92922) that is required for biological activity. FALL-39 is useful therapeutically for inhibiting microbial growth in mammmals, including humans, and is non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPBDCDFKKDGLVKRCMGTVTLNQARGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transplant; antimicrobial peptide; pore forming agent; cardioplegia; cell surface receptor binding compound; kidney transplant; cardioplegia; organ transplant; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                 antibiotic, FALL-39 - overcomes classical antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 874; DB 2; Length 170;
Pred. No. 1.4e-88;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transplant media associated antimicrobial peptide #32
                                                                                         Gunne H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU90996 standard; peptide; 170 AA
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                                                                                                                                                                                                  resistance and is non-cytotoxic.
                                                                                                                                                                                                                                      Example 2; Fig 1; 26pp; English
                                                                                       Gudmundsson GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.4%;
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17-NOV-2000; 2000US-0249602P.
15-MAY-2001; 2001US-0290932P.
                 94SE-00003055
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                                                                                                                          WPI; 1996-179899/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-268995/31
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Best Local Similarity
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                                                                                                                                             N-PSDB; AAT18233
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 170 AA;
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                                                     (BOMA/) BOMAN
                                                                                                                                                                                 peptide
                                                                                       Agerberth B,
                 13-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                        cytotoxic
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                                                                                                                                                                                                                                                                                                       The invention relates to a novel polypeptide composition for preventing disease in an organism which comprises one or more types of polypeptide which have an alpha-helix structure and/or thionine component. The composition of the invention demonstrates antibacterial and antifungal activities and may be useful for preventing a disease in an organism, for generating cultivated plants and in providing resistance to plant tissue against fungi such as Pyricularia oryzae (rice blast fungus), Ceratocystis finbriata and bacteria such as Pseudomonas etc. The composition has high antimicrobial activity at low concentration. The current sequence is that of the rabbit CAP18 full-length protein of the
                                                                                                                                                                                                      one
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                                                                                                                                                                                              Antimicrobial polypeptide composition for a plant pathogen, comprises or more types of thionine and/or a polypeptide having an alpha helix structure, as an active ingredient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.5%; Score 875; DB 8; L
Best Local Similarity 100.0%; Pred. No. 1.1e-88;
Matches 169; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 38; 27pp; Japanese.
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/label=_Prepro-peptide
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                                                                                                                        (TOYW ) TOYOTA CHUO KENKYUSHO
                                                   15-JAN-2002; 2002JP-00006607
                                                                                     15-JAN-2002; 2002JP-0006607
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                                                                                                                                                              WPI; 2004-102620/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 169 AA;
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                 22-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
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Thorton SL;

Hirsch R,

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The invention describes new transplant compositions comprising antimicrobial polypeptides or pore forming agents and/or cell surface antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds. The media is capable of extending the preservation period past 72 hours and can provide organs with increased functionality upon transplant. animals receiving kidneys stored in the media of the present invention for either three or four days had serum creatinine levels of less than half of those observed in control animals receiving kidneys stored in UW solution (defined in the specification) alone. Lower serum creatinine levels are indicative of healthier kidneys alone. Lower serum creatinine levels are indicative of healthier kidneys alone. Lower serum engelul for decreasing transplant of healthier kidneys and/or treated in the media. The media may also be used in procedures and/or treated in the media. The media may also be used in procedures and/or treated in the media. The media may also be used in procedures organs leads to a decrease in chronic rejection. This sequence represents an antimicrobial peptide studied in the development of the transplant
                         Media comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds useful for the storage and preservation of organs prior to transplant.
                                                                                                                                                 Disclosure; Page 27; 78pp; English.
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                                                     1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                            1 MKTORNGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                                                        LDPRPTMDGDPDTPKPVSPTVKETVCPRTTQQSPEDCDPKKDGLVKRCMGTVTLNQARGS
                          Gaps
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                                                                                                                                                            PDISCDKDNKRPALLGDPPRKSKEKIGKEFKRIVQRIKDPLRNLVPRTES 170
 Length 170;
                          Indels
Score 874; DB 5; Le
Pred. No. 1.4e-88;
1; Mismatches 0;
  99.44;
            99.48;
            Local Similarity 99.4
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Query Match
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autoimmune disease; arthritide; gene expression analysis; rheumatici arthritis; collagen-induced; immunosuppressive; antirheumatic; antiarthritis; osteopethic; antigout; antiinfiammatory; dermatological; immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibrosytis; ichomyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis; Human cathelicidin antimicrobial peptide. ADP65263 standard; protein; 170 AA (first entry) immune; human Homo sapiens 12-AUG-2004 ADP65263; RESULT 10 ADP65263 XX AC ADP(XX ADP(X

(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT. 31-OCT-2001; 2001US-0336220P. 31-OCT-2002; 2002WO-US035433. WO2003072827-A1. 04-SEP-2003

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The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using that that can expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention of turther comprises: a treatment of theumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis; dentification of array or gene chip, specific for rheumatoid arthritis; diagnosis or array or gene chip, specific for rheumatoid arthritis; accening the carray or gene chip, specific for rheumatoid arthritis; screening the carray or analyses of autoimmune disease or rheumatoid arthritis; screening the cefficacy of a candidate drug in vitro for the treatment of collagentinduced arthritis. The compositions of the invention have the following correctivities: immunosuppressive, antirheumatic, antiathritis, oscepathic, antishlammatory, dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease or arthritides, such as theumatoid arthritis, lupus, ankylosing spondylitis, fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and sease caused by an infectious agent. This sequence reparement of immune disease or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from
                                                                                                                               Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
                                                                                                                                                                                                                                                                              Disclosure; Page; 56pp; English.
                                                    2003-712740/67.
                                                                              GENBANK, NP_004336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 170 AA;
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120 61 LDPRPIMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120 9 9 LDPRPTMDGDPDTPKPVSFTVKBTVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD Gaps ö PDISCDKDNKRPALLGDPFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES Length 170, 0; Indels Score 874; DB 7; Pred. No. 1.4e-88; 1; Mismatches 0 99.4%; Best Local Similarity 99.4 Matches 169; Conservative 121 19 Query Match 8 음 셤 ਨੇ ò

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infection, cathelicidin type peptide; LL-37; antimicrobial; antiinflammatory; immunostimulant; bacterial infection; neutropenia; toothpaste; mouthwash; gingivitis; oral infection; periodontitls; human. ADN41827 standard; protein; 170 Human LL-37 protein SEQ ID NO:2. 15-JUL-2004 (first entry) ADN41827; 121 RESULT 11 ADN41827 ID ADN 유

Homo sapiens

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                                                                                                                                                                                                                                                                                          The present invention describes a method for determining the susceptibility of a subject to infection. The method comprises: (i) providing a sample from a subject; (ii) detecting any cathelicidin type providing a sample from a subject; (iii) detecting any cathelicidin type comparing the sample from the sample; (iii) optionally comparing the susceptibility of the subject to infection (where no LL-37 or a low level of LL-37 indicates that subject is susceptible to infection); and (v) optionally administering an antimicrobial agent to reduce infection. Also described is a product containing LL-37 and a cytostatic drug, corticosteroid or growth factor (preferably recombinant granulocyte colony stimulating factor (GCSP) or GM-CSP). The product has antimicrobial, antiinflammatory and immunostimulant activities. The method can be used for determining the susceptibility of a subject to infection such as bacterial infection (e.g. Actinobacillus actinomycetemcomitans infection) and neutropenia, and for diagnosing controls the normal flora in the form of toothpaste or mouthwash for the preventative treatment of infection e.g. contropenia and so combat lifections. The method controls the normal flora in neutropenia and so combat lifections. The present sequence represents the proform of human LL-37, which is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKTQRNGHSLGRWSLVILLILGLVWPLAIIAQVLSYKGAVLRAIDGINQRSSDANLYRLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                 Determination of susceptibility of subject to infection comprising
                                                                                                                                                                                                                               detecting cathelicidin type peptide present in sample, optionally comparing level of peptide in sample to control sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDISCDKDNKRFALLGDFFRKSKEKIGKBFKRIVQRIKDFLRNLVPRTES 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.4%; Score 874; DB 8; Length 17: 99.4%; Pred. No. 1.4e-88; ive 1; Mismatches 0; Indels
                                                                                                                                              Carlsson G;
                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 2; 40pp; English.
                                                                                                                                                Puetsep K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABM80449 standard; protein; 170 AA
                                                                10-OCT-2003; 2003WO-EP011240.
                                                                                           10-OCT-2002; 2002GB-00023655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 169; Conservative
                                                                                                                                               Boman H, Andersson M,
                                                                                                                                                                          2004-364936/34.
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Best Local Similarity
                                                                                                                    (MABT-) MABTECH AB
                                                                                                                                                                                        N-PSDB; ADN41826.
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            WO2004034061-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-2004
                                     22-APR-2004
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Delypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus server as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide commands. The invention also relates to nucleic acid and polypeptide compared to the TAT nucleic acid and nucleic acids and polypeptide; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; desponsitions are useful acid; an antibody specific for a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagoniers, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with concers, lung cancer, colorectes such expects. Colorected cancer, lung cancer, cervical cancer, inver cancer, bladder cancer, pancreatic cancer, cervical cancer, inverse system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and each and present sequence chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LDPRPTMDGDPDTPKPVSFTVKBTVCPRTTQQSPBDCDFKKDGLVKRCMGTVTLMQARGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human tumour-associated antigenic target (TAT)
           cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDPRPTMDGDPDTPKPVSFTVKBTVCPRTTQQSPBDCDFKKDGLVKRCMGTVTLNQARGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acids,
Tumour-associated antigenic target; TAT; human; overexpression; ci
tumour; diagnosis; cell proliferative disorder; breast cancer;
colorectal cancer; lung cancer; ovarian cancer; liver cancer;
central nervous system cancer; bladder cancer; pancreatic cancer;
cervical cancer; melanoma; leukaemia; hybridisation probe;
chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful in preparing a medicament for treating or detecting a
proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDISCOKONKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDISCDKDNYRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New tumor-associated antigenic target polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; SEQ ID NO 1129; 7273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2002; 2002US-0414971P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-SEP-2003; 2003WO-US028547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostate cancer or tumor.
                                                                                                                                                                                                                                    gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-347921/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ACN37923
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                                                                                                                                                                                                                                                                                                                                                                               WO2004030615-A2
                                                                                                                                                                                                                                                                                                             Homo sapiens.
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keratinocyte growth factor-2 (KGP-2) (1) comprising heterologous keratinocyte growth factor-2 (KGP-2) (1) comprising providing a host cell (1) consisting of primary keratinocytes and immortalized keratinocytes and an expression vector comprising a DNA sequence encoding (1) operably comprising (11) under conditions such that (1) is expressed.

(11), and culturing (11) under conditions such that (1) is expressed.

(2) Also described are: (11) produced by the novel method; a composition comprising keratinocyte specific promoter operably linked to a DNA comprising a keratinocyte specific promoter operably linked to a DNA comprising the vector; a method for providing a kin equivalent expressing an exogenous antimicrobial polypeptide; a host cell, which comprises the vector; a method for providing a kin equivalent expressing an exogenous antimicrobial polypeptide; a composition comprises the vector; a method for providing a state expressing an exogenous antimicrobial polypeptide; a method of selecting cells with increased pluripotency or multipotency relative to a population of comprising providing a population of cells and electroporating the cells generated by the method; a population of cells generated by the method; a population of cells generated by the method; a population of cells generated by the method; a method of selecting keratinocytes with holoclone or meroclone cell morphology comprises providing a population of cells generated by the method; a method of selecting keratinocytes with comphology are selected; and a keratinocyte population generated by the method; and a keratinocyte population generated by the method; and a keratinocyte population generated by the method; and a keratinocyte population generated by the complex wounds and a vector of an expective under conditions cell morphology are selected; and a keratinocyte population generated by the conditions of cells generated by the method; and a keratinocyte population generated by the conditions cell morphology are selected; and a keratinocyte pop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Providing cells expressing heterologous keratinocyte growth factor-2 (I), which is useful to treat wounds e.g. ulcerative colitis, comprises introducing a vector comprising a DNA that encodes (I) to a host cell and culturing the host cell.
                                                                                                                                                                                                                    vulnerary; antiulcer; antiinflammatory; gastrointestinal-gen.;
expression; vector; wound healing; vulnerary; injury; antimicrobial.
                                                                                                                                                                           Cathelicidin antimicrobial peptide SEQ ID NO 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 47; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antimicrobial peptide of the invention.
                                         ADX08374 standard; protein; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Centanni JM, Allen-Hoffmann L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003US-0491869P.
2003US-0493664P.
51US-00493664.
                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-2004; 2004WO-US024627
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (STRA-) STRATATECH CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-142888/15.
                                                                                                                                                                                                                                                                                                                                 WO2005012492-A2
                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-2003;
                                                                                                                               21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                             10-FEB-2005.
                                                                                      ADX08374;
RESULT 13
                      ADX08374
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Sequence 170 AA;

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LDPRPTWDGDPDTPKPVSFTVKETVCPRTTQQSPBDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of inhibiting the spread and/or reducing the risk of infection of a virus, involving contacting a virus with a cathelicidin functional fragment. The invention also relates to a method of treating atopic dermatitis involving contacting a subject having or suspected of having acopic dermatitis with an inhibiting effective amount of a cathelicidin functional fragment. The cathelicidin functional argument. The cathelicidin antiviral activity. The methods are useful for inhibiting the spread and/or reducing the risk of infection of a virus and for treating atopic dermatitis. This sequence represents the human cathelicidin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting spread and/or reducing risk of infection of virus, involves contacting virus with cathelicidin functional fragment.
                                                                                         1 MKTQRNGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                  LDPRPTWDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS
                                                                  1 MKTQRDGHSLGRWSLVLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                              Infection, viral infection, cathelicidin; atopic dermatitis; antimicrobial; virucide; dermatological; dermatological disease; immune disorder; inflammation.
                                                                                                                                                                                                     170
                                                                                                                                                                                                                      PDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
                                  ö
                                                                                                                                                                                                     PDISCDKDNKRPALLGDPPRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES
 Length 170;
99.4%; Score 874; DB 9; Length 17
99.4%; Pred. No. 1.4e-88;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note≈ "Encoded by GAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 6; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
(NAJE-) NAT JEWISH MEDICAL & RES CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    ADZ80363 standard; protein; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leung DYM;
                                                                                                                                                                                                                                                                                                                                                                                                                    Human cathelicidin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-OCT-2004; 2004WO-US034948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-OCT-2003; 2003US-0512953P.
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                    Best Local Similarity 99.4
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallo R, Murakami M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-355820/36.
                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2005040201-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                     14-JUL-2005
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     Query Match
                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                       ADZ80363
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                                                                                                                                                     61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                  LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine for active immunization or for preparing an adjuvant for enhancing an immune response to at least one antigen, comprises at least one antigen and at least one cathelicidin derived antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine, cathelicidin; antimicrobial; immunostimulant; immune response; antigen presenting cell; adjuvant; human; antibiotic; FALL-39.
                                                                                   1 WKTQRNGHSLGRWSLVLLLLGLVWPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
                                                                1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD
                                  Gaps
                                                                                                                                                                                                                     121 PDISCDKDNKRPALLGDPPRKSKEKIGKBPKRIVQRIKDFLRNLVPRTBS 170
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 Length 170;
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Pred. No. 1.4e-87;
                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buschle M, Egyed A;
                                                                                                                                                                                                                                                                                                                                                                                                                        Human peptide antibiotic FALL-39 precursor sequence.
99.4%; Score 874; DB 9;
ilarity 99.4%; Pred. No. 1.4e-88;
Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CIST-) CISTEM BIOTECHNOLOGIES GMBH
                                                                                                                                                                                                                                                                                                                     ABB07707 standard; peptide; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 1; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fritz J, Mattner F, Zauner W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.4%;
98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Query Match
Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 170 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                    ABB07707;
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Best Local S
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Matches 168; Conservative

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121 PDISCDKONKRFALLGDFFRKSKEKIGKBFKRIVQRIKDELRNLVPRTES 170 PDISCDKONKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170 61 61 121 ઠ 셤 ò g

Search completed: January 12, 2006, 21:48:09 Job time : 92.3321 secs

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GenCore version 5.1.6
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Bw model - protein search, using OM protein

Run on:

2006, 21:43:14 ; Search time 15.0554 Seconds (without alignments) 1086.448 Million cell updates/sec January 12,

Perfect score:

US-10-815-562-2 879 1 MKTQRDGHSLGRWSLVLLLL......KRIVQRIKDFLRNLVPRTES 170 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB M

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
!: pir1:*
: pir2:*
: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	CAP18 precursor -	antibacterial pept	ಹ	antibacterial pept	antibacterial prot		antimicrobial pept	elat	prophenin (PF-2) p	precur	antimicrobial prot	protegrin 5 precur	~	m	-	4	bactenecin 5 precu	cathelin-related p	indolicidin precur	myeloid antimicrob	cathelin-related p	cathelin-like anti	antimicrobial pept	cathelin - pig	polymorphonuclear	polymorphonuclear	secreted phosphopr	kininogen, LMW II	kininogen, HMW II
SUMMARIES	ID	138932	874248	JQ1171	268967	841731	A53421	868229	S70521	S40463	S27018	S68232	857609	0060NL	A53895	S57607	B53895	A45328	S68412	JC1222	S68228	S68411	S57330	S68230	XKPGC	B46634	A46634	I46051	KGBOL2	KGBOH2
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	Query Match Length	170	170	171	167	166	153	155	173	228	155	172	149	147	149	149	149	176	160	144	160	152	212	190	96	135	- 137	200	434	619
a	Query Match	100.0	99.4	53.0	50.6	50.5	49.9	49.2	49.1	48.9	48.6	48.6	48.3	47.6	47.6	47.6	47.6	46.7	46.2	46.1	45.4	45.1	44.1	42.6	36.3	19.6	19.5	7.6	9.7	9.7
	Score	879	874	465.5	444.5	443.5	438.5	432.5	431.5	429.5	427.5	427.5	424.5	418.5	418.5	418.5	418.5	410.5	406	405.5	399	396	387.5	374.5	319	172.5	171.5	85.5	85	82
	Result No.	H	7	e	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

kininogen, LMW I p	kininogen, HMW I p	hypothetical prote	spp-24 precursor -	hypothetical prote	lipoxygenase (EC 1	serine/threonine p	ATPase 2 (EC 3.6.1	hypothetical prote	£22b7.6 protein -	CTP synthetase ctr	hypothetical prote	hypothetical prote	FixL Oxygen regula	nitrogen fixation	hypothetical prote
KGBOL1	KGBOH1	AC1435	G01654	C84397	A53054	T50802	T31112	T18804	S44637	H84123	T20566	F84680	F95345	S39984	T15854
н	н	N	~	N	N	7	~	~	N	~	~	~	N	N	~
436	621	273	211	263	923	445	1082	444	518	532	2911	245	505	505	1599
9.6	9.6	4.6	9.3	9.0	9.0	6.8	8.9	8.8	8.8	8.8	8.8	8.7	8.5	8.5	8.5
84	84	82.5	82	79	79	78.5	78.5	77.5	77	77	77	76.5	75	75	75
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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CAPIS precursor - human Chapter (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Accession: 138932
R.Larrick, J.W.; Hirata, M.; Balint, R.F.; Lee, J.; Zhong, J.; Wright, S.C.
Infect. Immun. 63, 1299-1297, 1995
A.Title: Human CAPIS: a novel antimicrobial lipopolysaccharide-binding protein.
A.Reference number: 138932
A.Accession: 138932
A.Accession: 138932
A.Steatus: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type:
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ô Gapa ö Length 170; Indele 0 Query Match 100.0%; Score 879; DB 2; Best Local Similarity 100.0%; Pred. No. 8.8e-77; Matches 170; Conservative 0; Mismatches 0;

1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD

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120 61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120 9 1 MKTQRDGHSLGRWSLVLLLGLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPBDCDPKKDGLVKRCMGTVTLNQARGS 61 셤 g ò

121 FDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170 121 PDISCDXDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170 셤 ઠે

RESULT 2

Alternate names: antibacterial peptide LL-37 precursor - human NyAlternate names: antibacterial peptide FALL39
NyAlternate names: antibacterial peptide FALL39
NyContains: antibacterial peptide LL-37; cathelin-related antibacterial peptide CAP-18
C; poseites: Homo sapiens (man)
C; pate: 29-Jan-1998 #sequence revision 06-Feb-1998 #text_change 09-Jul-2004
N; Gddmundsson, G.H.; Agerberth, B.; Odeberg, J.; Bergman, T.; Olsson, B.; Salcedo, R.
Eur. J. Biochem. 238, 325-332, 1996
A; Title: The human gene FALL39 and processing of the cathelin precursor to the antibacte A; Reference number: S74248; MUID:96283824; PMID:8681941
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-170 cGUD>
A; Residues: 1-170 cGUD>
A; Residues: 1-170 cGUD>
A; Accession: S78211

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A;Note: 157-Asp was also found
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Best Local Si
Matches 98;
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          A MOLECULE CYPE: DIOCEAIN
A FREEdidues: 1141-143 GGUS-
A Crose-references: UNIPARC:UP1000017636D
A; Crose-references: UNIPARC:UP1000017636D
B; COWDard, J. B.; Johnsen, A.H.; Borregaard, N.
B; Crose-references: UNIPARC:UP1000000067; PMID: 7615076
A; Reference number: S66205; MUD: 95339969; PMID: 7615076
A; Residues: 1-12, T', 114-170 < COW>
A; Residues: 1-12, T', 114-170
A; Residues: 1-12, T', 114-170
A; Residues: 1-12, T', 114-120
A; Residues: 10-12, T', 114-170
A; Residues: 10-12, T', 114-1
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Nyllernate names: 18K cationic protein
C;Specias: Orytoolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996
C;Accession: JQ1171; PS0226
C;Accession: JQ1171; PS0226
C;Accession: JQ1171; PS0226
C;Accession: JQ1171; PS0226
R;Larrick, J.W.; Morgan, J.G.; Palings, I.; Hirata, M.; Yen, M.H.
Biochem. Blophys. Res. Commun. 179, 170-175, 1991
A;Reference number: JQ1171; MUD:91354246; PMID:1883348
A;Accession: JQ1171; MUD:91354246; PMID:1883348
A;Accession: JQ1171 MUD:91354246; PMID:1883348
A;Accession: Sp0226
A;Molecule type: mRNA
A;Accession: PS0226
A;Molecule type: protein
A;Residues: 135-159; OGGQLL' <LA2>
A;Cross-references: UNIPARC:UPI0000176372
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99.4%; Score 874; DB 2;
Best Local Similarity 99.4%; Pred. No. 2.7e-76;
Matches 169; Conservative 0; Mismatches 1;
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antibaterial peptide - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus Scrofa domestica (domestic pig)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: 568967
R;Tossi, A.; Scocchi, M.; Zanetti, M.; Storici, P.; Gennaro, R.
R;Tossi, A.; Scocchi, M.; Zanetti, M.; Storici, P.; Gennaro, R.
R;Tossi, A.; Scocchi, M.; Zanetti, M.; Storici, P.; Gennaro, R.
R;Tossi, A.; Scocchi, M.; Zanetti, M.; Storici, P.; Gennaro, R.
A;Reference number: 568967
A;Reference number: 568967; MUID:95255306; PMID:7737198
A;Accession: Scassor
A;Accession: preliminary
A;Molecule type: mRNA
A;Residues: 1-167 <TOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P49932; UNIPARC:UPI000012F429; EMBL:L39641; NID:g703244; PID:
C;Superfamily: cathelin; cystatin homology
F;22-129/Domain: cystatin homology <CYS>
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C;Species: Sus scroca domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: 841731
R;Storici, P.; Scocchi, M.; Tossi, A.; Gennaro, R.; Zanetti, M.
R;Storici, P.; 303-307, 1994
A;Title: Chemical synthesis and biological activity of a novel antibacterial peptide ded
A;Reference number: $41731; MUID:94123775; PMID:8293820
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A,Residues 1.166 «STO»
A;Gross-references: UNIRROT:P49931; UNIPARC:UPI000012F428; GB:L29125; NID:g457347; PIDN:
C;Superfamily: cathelin; cystatin homology
C;Superfamily: cathelin; cystatin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>
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120 LDITCNBIQSVGLLSRLRDFLSDRGRRLGEKIBRIGQKIKD 160
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                                                                                                                                             ch 53.0%; Score 465.5; DB 2
1 Similarity 57.3%; Pred. No. 3.5e-37;
98; Conservative 26; Mismatches 44
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cathelin-related protein precursor - mouse (1) pacing musculus (house mouse) (1) pacies: Mus musculus (house mouse) (2) pate: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 (2) Accession: 870521 (3) Pacing M.V.; Visser, J.W.; Zijlmans, J.M.J.M.; Fibbe, W.E.; Bely Fregsueva, A.E.; Zinovjeva, M.V.; Visser, J.W.A.; Zijlmans, J.M.J.M.; Fibbe, W.E.; Bely A;Title: A novel murine cathelin-like protein expressed in bone marrow. A;Reference number: 870521; MUID:96326596; PMID:8706928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Reaidues: 1-173 < POP>
A, Reaidues: 1-173 < POP>
A, Cross-references: UNIPROT: P51437; UNIPARC: UPI0000049482; EMBL: X94353; NID: 91177533; PI C, Superfemily: cathelin; cystatin homology
F; 1-23/Domain: signal sequence #status predicted <SIG>F; 24-144/Domain: propeptide #status predicted <PRO>F; 1-23/Product: cathelin-related protein #status predicted <MAT>
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NyAlternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor
NyAlternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 840463; 857331; §6823
R;Pungercar, J; Strukelj, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, P.; Turk,
PEBS Lett. 336, 284-288, 1993
A;Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial
A;Reference number: 840463; MUID:94085623; PMID:8262247
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                                                                                       Length 155;
F;22-129/Domain: cystatin homology <CYS>
F;29-143/Domain: propeptide #status predicted <PRO>
F;144-155/Product: antimicrobial peptide #status predicted <MAT>
                                                                                                                                      Indela
                                                                                                                                      21;
                                                                                         DB 2;
                                                                                                               ; Pred. No. 4.5e-34; 18; Mismatches 21
                                                                                            Score 432.5;
                                                                                         49.2%;
                                                                                                                 68.3%;
                                                                                  Query Match
Best Local Similarity 68.3%
Matches 86; Conservative
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120 FDITCN 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary A;Molecule type: mRNA
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A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     A53421
antibacterial peptide precursor - pig
antibacterial peptide precursor - pig
antibacterial peptide domestica (domestic pig)
C; Species: Sus Scrofa domestica (domestic pig)
C; Date: 19-May-1994 #text_change 09-Jul-2004
C; Accession: A53421
R; Zanetti, M: Storici, P:; Tossi, A.; Scocchi, M.; Gennaro, R.
J. Biol. Chem. 269, 7855-7858, 1994
A; Title: Molecular cloning and chemical synthesis of a novel antibacterial peptide deriv
A; Reference number: A53421; MUID:94179144; PMID:8132502
A; Accession: A53421
A; Ratus: preliminary
A; Molecule type: mRNA
A; Readus: 1-153 < ZAN
A; Cossion: C; Superfamily: cathelin; cystatin homology
C; Superfamily: cathelin; cystatin homology
C; Keywords: antibacterial
F; 22-129/ Domain: cystatin homology < CYS>
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                                                                                         <u>ب</u>
                                                 Length 166;
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                                          Query Match 50.5%; Score 443.5; DB 2; Best Local Similarity 61.3%; Pred. No. 4.3e-35; Matches 95; Conservative 18; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                 120 LDINCDEIOSVGRFRRLRKKTRKRLKKIGKVLKWI 154
                                                                                                                                                                                                                                                                                                                       PDISCDKDNK--RFALLGDFPRKSKEKIGKEFKRI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 67.7%; Pred. No. 1.2e-34;
Matches 86; Conservative 19; Mismatches 21
  F;22-129/Domain: cystatin homology <CYS>
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FDITCNQ 126
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P;144-155/Product: bactenecin #status experimental <MAT>
P;146-154/Disulfide bonds: #status experimental
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A;Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V. Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
A;Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte A;Reference number: S57330; MUID:96042752; PMID:7576250
A;Accession: S57331
A;Status: preliminary
A;Molecule type: mANA
A;Residues: 1-228 «STR»
A;Cross-references: UNIPARC:UPI0000131713
B;Zhao, C.; Ganz, T.; Lehrer, R.I.
FRBS Lett. 376, 130-134, 1995
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: propher A;Reference number: S68233; MUID:96105365; PMID:7498526
A;Accession: S68233
A;Reference number: S68232; MUID:96105365; PMID:7498526
A;Accession: S68233
A;Residues: 1-228 «ZHA»
A;Residues: 1-228 «ZHA»
A;Residues: 1-228 «ZHA»
A;Residues: 1-229 «ZHA»
A;Residues: Cystatin homology
C;Superfamily: cathellin; cystatin homology «CYS»
F;22-129/Domain: cystatin homology «CYS»
F;30-228/Product: prophenin (PF-2) #status predicted «MAT»
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Bactenedin precursor - bovine

NyAlternate names antibiotic dodecapeptide
C;Species: Bos primigabilus taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Date: 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Date: 32-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: 327018; A33799
R;Storici, P.; del Sal, G.; Schneider, C.; Zanetti, M.
R;Storici, P.; del Sal, G.; Schneider, C.; Zanetti, M.
R;Storici, P.; del Sal, MID:93093170; PMID:1459251
A;Title: CDMA sequence analysis of an antibiotic dodecapeptide from neutrophils.
A;Residues: 1-155 csTo.
A;R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 LDITCNEGVRRFFWWWPFLRRPR 142
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A,Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen A,Reference number: S68232; MUID:96105365; PMID:7498526
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A;Status: translation not shown
A;Molecule type: DNA
A;Mosidues: 1-17-<2HA>
A;Rosidues: 1-17-<2HA>
A;Cross-references: UNIPROT:P80054; UNIPARC:UPI000013215A; EMBL:X89201; NID:gl165150; PI
A;Experimental source: leukocytes
R;Storici, P:; Zanetti, M.
Biochem. Biophys: Res. Commun. 196, 1058-1065, 1993
A;Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the A;Reference number: JN0899; MUID:94071853; PMID:8250863
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A, Molecule type: mRNA
A, Residues: 1-20, A', 22-172 <STO>
A, Residues: 1-20, A', 22-172 <STO>
A, Residues: 1-20, A', 22-172 <STO>
A, Conserved the marrow cells
A, Experimental source: bone marrow cells
R, Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bom Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
A, Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fam A, Reference number: 147138, MUID:95350216; PMID:7624374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA, CPA60682.1; PI A; Molecule to the type: Lee, J.Y.; Dergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall R; Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall Bur. J. Biochem. 202, 849-854, 1991
A; Title Amino acid sequence of PR-39. Isolation from pig intestine of a new member of the A; Reference number: S19563; MUID:92111534; PMID:1765098
                                                                                                                                                                                                                                                                                                                          61 LDPRPTMDGDPDTPKPVSFTVKBTVCPRTTQQSPBDCDPKXDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                                                                                                                                        60 LDQPPQDDEDPDSPKRVSFRVKETVCSRTTQQPPEQCDFKENGLLKRCEGTVTLDQVRGN 119
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NiAlternate names: myeloid antibacterial protein PR-39
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cibace: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
Cibacesion: S68232; JN0899; I47138; S19563
RiZhao, C.; Ganz, T.; Lehrer, R.I.
RiZhao, C.; Ganz, T.; Lehrer, R.I.
A;Title: Structures of genes for two cathelin-associated antimicrobial pepti
                                                                                                                                                               1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                         Gaps
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Cisuperfamily: cathelin; cystatin homology
Cisuperfamily: cathelin; cystatin homology
Ciscywords: amidated carboxyl end; antibacterial
Fil-29/Domain: signal sequence #status predicted <SIG>
Fi22-129/Domain: cystatin homology <CXS>
Fi30-130/Domain: propeptide #status predicted <PRO>
Fi30-130/Domain: propeptide #status predicted <PRO>
Fi31-169/Product: antimicrobalal protein PR-39 #status experimental <MAT>
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;
    Length 155;
                                                                               Indels
                                                                               23;
    DB 2;
                                              Pred. No. 1.4e-33;
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                                                                           18; Mismatches
        Score 427.5;
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A;Cross-references: UNIPARC:UPI00002D613
A;Experimental source: intestine
        48.68;
                                              66.78;
                                                                               84; Conservative
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|20 FDITCN 125
Query Match
Best Local Similarity
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                                                                                   Matches
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A;Cross-references: UNIPROT:P32195; UNIPARC:UPI0000131776; GB:L24745; NID:9431435; PIDN: R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, RESE Lett. 330, 339-342, 1993
A;Title: Primary structure of three cationic peptides from porcine neutrophile. Sequence A;Reference number: S36820; MUID:93387466; PMID:8375505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rikokryakov, V.N.; Harwig, S.S.L.; Panyutich, B.A.; Shevchenko, A.A.; Aleshina, G.M.; Sh BRS Lett. 327, 231-236, 1993
Afitle: Protegrins: leukocyte antimicrobial peptides that combine features of corticost A; Reference number: S34585; MUID:93327946; PMID:8335113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 131-146 < KOK>
A; Residues: 131-146 < KOK>
A; Residues: 131-146 < KOK>
A; Cross-references: UNIPARC:UP1000014310F
A; Cross-references: UNIPARC:UP1000014310F
C; Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism C; Superfamily: cathelin; cystatin homology
C; Keywords: amidated carboxyl end; antibacterial; neutrophil
F; 1-29/Domain: signal sequence #status predicted < SIG>
F; 1-29/Domain: cystatin homology < CVTS>
F; 1-21-19/Domain: cystatin homology 

F; 1-13-146/Product: protegrin 2 #status experimental < MAT>
F; 1-146/Modified site: amidated carboxyl end (Val) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P32196; UNIPARC:UPI0000131777; EMBL:X84095; NID:g887644; PID R;Zhao, C.; Liu, L.; Lehrer, R.I. FEBS Lett. 346, 285-288, 1994
A;Title: 1dentification of a new member of the protegrin family by cDNA cloning. A;Reference number: 845712; MUID:94283613; PMID:8013647
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A;Cross-references: UNIPARC:UP10000131777; GB:X83267; NID:g603037; PIDN:CAA58240.1; PID:
K;Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, B.A.; Shevchenko, A.A.; Aleshina, G.M.; Sh
FEBS Lett. 327, 231-236, 1993
A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPBDCDFKKDGLVKRCMGTVTLNQARGS 120
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NiAlternate names: neutrophil peptide 2
CiSpecies: Sus scrofd domestics (domestic pig)
CiSpecies: Ol-Dec-1995 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004
CiDate: 01-Dec-1995 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004
CiAccession: S66285; A53895; S34587; S36821; S57608
Rizhao, C.; Ganz, T.; Lehrer, R.I.
REBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
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A;Reference number: S66283; MUD:95354835; PMID:7628604
A; Reference number: JN0900; MUID: 94071898; PMID: 8250892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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47.6%; Score 418.5; DB 2
Best Local Similarity 65.4%; Pred. No. 9.3e-33;
Matches 83; Conservative 19; Mismatches 24
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                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 131-146 <MIR>
A;Cross-references: UNIPARC:UPI000014310F
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120 LDITCNE 126
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A;Residues: 1-149 <ZH3>
                                                                                     A; Molecule type: mRNA
A; Residues: 1-147 <STO>
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S55609
protegrin 5 precursor - pig
N;Alternate names: cathelin-associated antimicrobial peptide
C;Species: Sus scrofa domestica (domestic pig)
C;Dacession: S6628; Baequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S6628; S7609
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FRES. Lett. 368, 199-1-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
A;Reference number: S66283; MUID:95354835; PMID:7628604
A;Reference number: S66283
A;Residues: 1-149 <ZHA>
A;Residues: 1-149 <ZHA
A;Residues: 1-149 <Z
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NiAlternate names: catchelin-like protein precursor; neutrophil peptide 3
SiAlternate names: catchelin-like protein precursor; neutrophil peptide 3
Cipaceis: Sus scrofa domestica (domestic pig)
Cipate: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
Cipacession: JN0900; S36822; S34586
Ristorioi, P.; Zanetti, M.
Biochem. Blophys. Res. Commun. 196, 1363-1368, 1993
A;Title: A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a cat
F;169/Modified site: amidated carboxyl end (Pro) (amide in mature form following gl
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48.3%; Score 424.5; DB 2; Length 149;
Best Local Similarity 66.1%; Pred. No. 2.5e-33;
Matches 84; Conservative 19; Mismatches 23; Indels 1.
                                                                                         DB 2; Length 172;
                                                                            Query Match 48.6%; Score 427.5; DB 2; Length Best Local Similarity 67.7%; Pred. No. 1.5e-33; Matches 86; Conservative 17; Mismatches 23; Indels
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|120 LDISCNE 126
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JN0900
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FEBS Lett. 327, 231-236, 1993
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A; Reference number: S34585; MUID:93327946; PMID:8335113
A; Accession: S34587
A; Accession: S34587
A; Accession: S34587
A; Molecule type: protein
A; Residues: 131-148 «KOX»
A; Cross-references: UNIPARC:UP10000143110
R; Mirgorodakaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, FBSS Lett. 330, 339-342, 1993
A; Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence A; Reference number: S36820; MUID:93387466; PMID:8375505
A; Reference number: S36820; MUID:93387466; PMID:8375505
A; Residues: 131-148 «MIR»
A; Residues: 131-148 «MIR»
A; Residues: UNIPARC:UP10000143110
C; Genetics:
A; Genetics:

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A; Casb-references: UNIPROT: P32194; UNIPARC: UP10000131775; EMBL: X84094; NID: G887642; PID
R; Zhao, C.; Liu, L.; Lehrer, R.I.
A; Accession: S45712
A; Reference number: S45712; MUID: 94283613; PMID: 8013647
A; Residues: 1-149 < ZH2>
A; Residues: S36820
A; Rocession: S36820
A; Residues: UNIPARC: UP10000034C2E
A; Residues: UNIPARC: UP1000034C2E
A; Residues: UNIPARC: UP1000034C2E
A; Residues: UNIPARC: UP1000034C2E
A; Residues: Lill-148 < ZHIA-
A; Residues: UNIPARC: UP1000034C2E
A; Rocession: R; Rokryakov, V.N.; Harwig, S.S.L.; Panyutich, B.A.; Shevchenko, A.A.; Aleshina, G.M.; SH
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NyAlternate names: neutrophil peptide 1
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Oct-1995 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S66284; S45712; $36820; S34585; S57607
R;Zhao, C; Ganz, T.; Lehrer, R.I.
FBES Lett. 368, 197-202, 197-202, 197-204
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
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A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost A;Reteance number: S34585; MUID:93327946; PMID:8335113
A;Accession: S34585
A;Accession: S34585
A;Accession: S34585
A;Accession: S34585
A;Accession: S34585
A;Accession: S34585
A;Coss-references: UNIPARC:UPIO000034C2E
A;Coss-references: UNIPARC:UPIO000034C2E
C;Genetics: A;Gene: NGC1
A;Introns: 66/3: 102/3: 126/3
A;Introns: 66/3: 126
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GenCore version 5.1.6
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OM protein - protein search, using sw model

January 12, 2006, 21:42:24; Search time 82.8044 Seconds (without alignments) 1448.471 Million cell updates/sec Run on:

US-10-815-562-2 879 1 MKTQRDGHSLGRWSLVLLLL......KRIVQRIKDFLRNLVPRTES 170 Title: Perfect score: Sequence:

Scoring table:

2166443 seqs, 705528306 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

2166443

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

otion	homo sapien	macaca mula	macaca mula	equus cabal	canis famil	oryctolagus	equus cabal	bos taurus	rattus norv	equus cabal	sus scrofa	sus scrofa				sus scrofa	ovis aries	mus musculu	ovis aries	bos taurus	bos taurus	capra hircu	sus scrofa	bos taurus	sus scrofa	bos taurus					
Description	P49913	Q71sn9	09g1v5	062841	Q6tn20	P25230	062842	P56425	Q71km5	062840	P49932	P49931	P82018	Q4 j fb9	P79360	P49930	P79362	P51437	P54230	P54228	P54229	P82017	P51525	P22226	P80054	P49934	P32195	P32194	P32196	P49933	P19661
SUMMALIES	FAL39 HUMAN	PAL39 MACMU	Q9GLV5 MACMU	O62841 HORSE	Q6TN20 CANFA	CAP18 RABIT	062842 HORSE	BMA34 BOVIN	Q71KM5 RAT	062840 HORSE	PMP37 PIG	PMP36 PIG	BCTN5 CAPHI	Q4JFB9 CAPHI	P79360_SHEEP	PMP23 PIG	BCTN5 SHEEP	CRAMP MOUSE	BCTN1 SHEEP	BMA27_BOVIN	BMA28 BOVIN	P82017_CAPHI	PF12_PIG	BCTN1 BOVIN	PR39 PIG	PG5_FIG	PG2_PIG	PG1_PIG	PG3_PIG	PG4_PIG	BCTN7_BOVIN
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* Query Match Length	170	170	170	157	172	171	170	165	171	156	167	166	176	176	165	153	176	173	155	158	159	165	228	155	172	149	147	149	149	149	190
Query Match	100.0	100.0	86.3	56.7	55.3	53.3	52.0	51.6	51.6	51.3	9.05	50.5	50.3	50.3	50.1	49.9	49.8	49.3	49.2	49.1	49.1	49.0	48.9	48.6	48.6	48.3	47.6	47.6	47.6	47.6	47.4
Score	879	879	759	498.5	486.5	468.5	457.5	454	453.5	451	444.5	443.5	442.5	442.5	440	438.5	437.5	433.5	432.5	432	432	431	429.5	427.5	427.5	424.5	418.5	418.5	418.5	418.5	416.5
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Q9xsq8 capra hircu P49928 ovis aries	P19660 bos taurus Q683r8 bubalus bub P33046 bos taurus	P49929 ovis aries P51524 sus scrofa	Q9xeq9 capra hircu P79361 ovis aries	P50415 ovis aries O19031 ovis aries	O19040 ovis aries Q91x12 cavia porce	Q920x4 mus spicile
O9XSQ8 CAPHI SC51_SHEEP	BCTN5 BOVIN Q683R8 BUBBU INDC_BOVIN	SC52 SHEEP PF11_PIG	Q9XSQ9_CAPHI P79361_SHEEP	BCTN7 SHEEP 019031 SHEEP	O19040_SHEEP Q91X12_CAVPO	Q920X4_MUSSI
77	- 7 F		~ ~	- 8	~ ~	N
158	176 144 144	160 212	190	190 224	182 178	109
47.0	46.7 46.2 46.1	45.5	43.9 43.3	42.6	41.0	36.7
413	410.5 406.5 405.5	400 387.5	385.5 380.5	374.5 369.5	360.5 325	322.5
33	8 8 8 4 8 9	37 38	39	4 4 4 2 4 2	4 4 6 4	45

ALIGNMENTS

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HGNC; HGNC:1472; CAMP.
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MUCLECTIDE SEQUENCE [LARGE SCALE MRNA].

MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUBDER R.D., Felngold R.A., Grouse L.H., Derge J.G.,

MISCHIL S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MISCHOLL, Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

MAR S.S., Loquellano N.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

MAR S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Myllalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Radesley S., Worley K.C., Sheckenko Y., Bouffard G.G.,

Makting M., Madan A., Young A.C., Sheckenko Y., Bouffard G.G.,

Matting M., Madan A., Young A.C., Sheckenko Y., Bouffard G.G.,

Matting M., Schimwod J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Schalska U., Smailus D.E.,

M. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

M. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

M. Butterfield Y.S.N., Krzywinski M.I., Shalska U., Smailus D.E.,

M. Bonards D.N. A. Schein J.E., Jones S.J.M., Marra M.A.;

M. Brander D.N. A. Schein J.E., Jones S.J.M., Marra M.A.,

M. Brander D.N. A. Schein J.E., Jones S.J.M., Marra M.A.,

M. Brander D.N. A. Schein J.E., Jones S.J.M., Marra M.A.,

M. Brander D.N. A. Schein J.E., Jones S.J.M., Marra M.A.,

M. Brander D.N. A. Schein J.E., Jones S.J.M., Marra M.A.,

M. Brander D.N. A. Schein J.E., Jones S.J.M., Marra M.A.,

M. Brander D.N. A. Schein J.E., Jones S.J.M., Marra M.A.,

M. Brander D.N. A. Schein J.E., Jones M.D., Marra M.A.,

M. Brander D.N. A. Schein J.E., Jones M.D., Marra M.A.,

M. Brander D. J. Brander D. Brand
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                                                                                                                                                                                                                                                                                                                                                                Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W., Koan B., Zuo D., Hu Y., Labaer J., "Cloning of human full open reading frames in Gateway (TM) system entry vector (pDONR201)."
"The human gene FALL39 and processing of the cathelin precursor to the antibacterial peptide LL-37 in granulocytes."; 
Eur. J. Biochem. 238:325-332(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has antibacterial activity.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed in bone marrow and testis and
                                                                                                                                                                                                                                                     Wu N., Miao S.Y., Zhang X.D., Qiao Y., Liang G., Wang L.F., "A new spermatogenesis-related gene.";
                                                                                                                                                                                                                                                                               "A new spermatogenesis-related gene.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                               IISSUE=Epididymis;
Gao Y., Huang Y.F., Xia X.Y.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases
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SIMILARITY: Belongs to the cathelicidin family.
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L; X89568; CAA61805.1; -; mRNA.
L; U19970; AAA70404.1; -; mRNA.
L; U48795; AAC02654.1; -; Genomic DNA.
L; X96735; -; NOT ANNOTATED CDS; Genomic_DNA.
L; AY162210; AAA703131.1; -; mRNA.
L; AX251531; AAA20054.1; -; mRNA.
L; CR457083; CAG33364.1; -; mRNA.
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PIR, S74248, S74248.
HSSP, B23196, 1KWI.
Ensembl, ENSG0000164047, Homo saplens.
                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
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EMBL; BC055089; AAH55089.1; -; mRNA
                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [MRNA].
                                                                                          NUCLEOTIDE SEQUENCE [MRNA]
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                     Antibacterial protein FALL-39.
Antibacterial protein LL-37.
Pyrrolidone carboxylic acid (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
When it Ref. 1, 6, 7 and 8; CAG46759).
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MEDLINE-21137962; PubMed-11238224; DOI-10.1128/CDLI.8.2.370-375.2001;
Bals R., Lang C., Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;
"Rhesus monkey (Macaca mulatta) mucosal antimicrobial peptides are
close homologues of human molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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113-SEP-2005 (Rel. 48, Last annotation update)
Antibacterial protein FALL-39 procusor (RALL-39 peptide antibiotic)
(Cationic antimicrobial protein CAP-18) (rhCAP-18) [Contains:
Antibacterial protein LL-37 (rhLL-37)].
Antibacterial protein RAL-37 (rhLL-37)].
Mame=CAMP; Synonyme=CAPLB; FALLL39;
Macaca mulatta (Rhesus macaque).
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 879; DB 1; Length 170; 100.0%; Pred. No. 6.9e-76;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                           InterPro; IPR001894; Cathelicidin.
PANTHER; PTHR10206; Cathelicidin; 1.
Prodom; PR001894; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Antibiotic; Antimicrobial; Direct protein sequencing; Pyrcolidone carboxylic acid; Signal.
SIGNAL
MIM; 600474; -.
GO; GO:0042742; P:defense response to bacteria; TAS.
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10-MAY-2005 (Rel. 47, Last seq
                                                                                                                                                                                                                                                                                                                                170 AA; 19301 MW;
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MEDLINE=21441139; PubMed=11557457;

MEDLINE=21441139; PubMed=11557457;

MEDLINE=21441139; PubMed=11557457;

Maring A., Lehrer R.I.;

Maring A., Lehrer R.I.;

"RL-37, an alpha-helical antimicrobial peptide of the rhesus monkey.";

Antimicrob. Agents Chemother. 45:2695-2702(2001).

EMBL: AF181954; AAG09440.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIJAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
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European Bioinformatics Institute. There are no restrictions o as long as its content is in no way modified and this statement
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                                                                                 EMBL; AF288284; AAG40802.1; -; mRNA.
InterPro; IPRO01894; Cathelicidin.
PANTHER; PTHR10206; Cathelicidin; 1.
Propom; PP00666; Cathelicidins; 1.
ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Antibiotic; Antimicrobial; Pyrrolidon; carboxylic acid; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0006952; P:defense response; IEA.
GO; GO:0006913; P:response to pest, pathogen or parasite; IEA.
InterPro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 879; DB 1; Length 170; 100.0%; Pred. No. 6.9e-76; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                   Antibacterial protein FALL-39. Antibacterial protein LL-37.
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PROSITE, PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00946; CATHELICIDINS 2; 1.
SEQUENCE 170 AA; 18861 MW; 355AB3BF510DB883 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         similarity).
055B07DCA95A7D16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 759; DB 2;
Pred. No. 2.1e-64;
                                                                                                                                                                                                                                                                                                   Potential.
                                                                                                                                                                                                                                                                            Potential
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                                                                                                                                                                                                                                                                                                                                                                                                            170 AA; 19301 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Matches 170; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                        61 LDPRPIMDGDPDTPKPVSFTVKETVCPRTTQKSPEDCDFKEDGLVKRCVGTVILNQARDS 120
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                                                                  1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
                                           1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Bone marrow;
MEDLINE=99402973; Pubmed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto B.,
Zanetti M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R Wovel catheliciding in horse leukocytes.";

FEBS Lett. 457:459-464(1999).

R REML, AJ224929. CAA12227.1; -; mRNA.

R HSSP; P32196; 1KWI.

R GO; GO:0005976; C:extracellular region; IEA.

R GO; GO:000513; P:response; IEA.

R GO; GO:0009613; P:response to peet, pathogen or parasite; IEA.

R FEMS PROSITE; PS001894; Cathelicidin.

R ProDom; PD001888; Cathelicidin; 1.

R PROSITE; PS00947; CATHELICIDINS_1; 1.
                                                                                                                                                                                                                        170
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Name-eCATH-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 56.7%; Score 498.5; DB 2; Local Similarity 76.4%; Pred. No. 1.7e-39; les 97; Conservative 13; Mismatches 16;
  12;
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  Mismatches
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  11;
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062841;
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ID QGTN20 CANFA PRELIMINARY;
AC QGTN20;
  Conservative
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157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQGSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
                                                                 Cathelicidin.
Canla familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Pissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A) [Contains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDISCDK--DNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTE 169
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ENBELL; AY392089; AR26545.1; -; mRNA.
Ensembl; ENGCAFG0000012896; Canis familiaris.
GO; GO:000555; P:defense response; IRA.
GO; GO:0009613; P:response to pest, pathogen or parasite; IRA.
InterPro; IRR001894; Cathelicidins.
Prom; PF00066; Cathelicidins; 1.
Probom; PD001838; Cathelicidins; 1.
SEQUENCE 172 AA; 19437 MW; 549EAC408DEB7A63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.3%; Score 486.5; DB 2; Length 172; 57.9%; Pred. No. 2.7e-38;
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Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I.,
Wilson D., Yen M.H., Wright S.C., Larrick J.W.;
"Characterization of a rabbit cationic protein (CAP18) with
lipopolysaccharide-inhibitory activity.";
Infect. Immun. 62:1421-1426(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;
"Complementary DNA sequence of rabbit CAP18 -- a unique
lipopolysaccharide binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Indels
                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
Sang Y., Rune K., Melgarejo T., Blecha F.;
Submitted (SRP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 135-159
  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 179:170-175(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Mismatches
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MEDLINE=91354246; PubMed=1883348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                 NCBI_TaxID=9615;
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P25230;
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CAP18 RAB
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ID CAP1 01-M
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The solution structure of the active domain of CAP18 -- a lipopolysaccharide binding protein from rabbit leukocytes."; FRBS Lett. 370:46-52(1995).
-!- FUNCTION: CAP18 binds to the lipid a moiety of bacterial lipopolysac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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PDB; ILYP; NMR; @=135-166.

InterPro; IPR001984; Cathelicidin.

PANTHER; PTHR10206; Cathelicidin; 1.

PEOMO; PD001838; Cathelicidin; 1.

PROSTIE; PS00946; CATHELICIDINS 1; 1.

PROSTIE; PS00947; CATHELICIDINS 2; 1.

3D-structure; Antiblotic; Antimicrobial; Direct protein sequencing; SIGNAL

SIGNAL

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 135-166.
MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8; Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F., Huang T.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 FDISCDK--DNKRPALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
               MEDLINE-94075827; PubMed-8254133;
Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D.,
Cavalllon J.-M., Warren H.S., Wright S.C.;
"A novel granulocyte-derived peptide with lipopolysaccharide-
neuralizing activity";
J. Immunol. 152:231-240(1994).
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Antimicrobial protein CAP7.
Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                      in CAP18, a lipopolysaccharide binding protein from rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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D7BF2103BCFB13C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
PROTEIN SEQUENCE OF 135-154, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
53.3%; Score 468.5; DB 1
Best Local Similarity 57.3%; Pred. No. 1.4e-36;
Matches 98; Conservative 27; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity)
                                                                                                                                                                                                                                                                                                                                                      FEBS Lett. 339:108-112(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19805 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171
171
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171 AA;
                                                                                                                                                                                                       CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
135
30
                                                                                                                                                                                                                                                                                                                                   leukocytes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Bone marrow;
MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE-98072398; PubMed=9409740; DOI=10.1016/S0014-5793(97)01310-0; Scocchi M., Wang S., Zanetti M.; Structural organization of the bovine cathelicidin gene family and identification of a novel member.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEBS Lett. 457:459-464 (1999).

RMBL; Al224929; CAA12228.1; -; mRNA.

RMSP; P23196; INWI.

SNR; O62842; 30-130.

GO; GO:00065276; C:extracellular region; IEA.

GO; GO:00065279; P:defense response; IEA.

RGO; GO:0006532; P:response to pest, pathogen or parasite; IEA.

InterPro: IPR001894; Cathelicidin.

Rfam; PF00066; Cathelicidins; 1.

RF0DOM; PS000946; CATHELICIDINS 1; 1.

RROSITE; PS00946; CATHELICIDINS 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Bukaryota, Metazota, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia;
Pecora, Bovidae, Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E., Zanetti M.; "Novel cathelicidins in horse leukocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDISCDKDN--KRFALLGDFPRKSKEKIGKEFK-----RIVQRIK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 PDASCDEPQRVKRFHSVGSLIQRHQQMIRDKSEATRHGIRIITRPK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myeloid cathelicidin 3.
5C35F1FA2D112BC8 CRC64;
                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Myeloid cathelicidin 3 precursor.
Name=eCATH-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.0%; Score 457.5; DB 2
57.2%; Pred. No. 1.6e-35;
iive 24; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2005 (Rel. 48, Last annotation update)
Antibacterial peptide BMAP-34 precursor.
                                                    170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
                                                    PRT;
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                                               O62842 HORSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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170
                                                                                                                                                                                                                                                                                                                                                                                                             Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
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les 95; Conserv
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NCBI_TaxID=9913;
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P56425;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 LDPPPEQDVEHPGARKPVSFTVKETVCPRTTPQPPEQCDFKENGLVKQCVGTVTRYWIRG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                    -!- FUNCTION: Exerts a potent antimicrobial activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cartus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; P0001838; Cathelicidin; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Amidation; Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid;
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Termen S., Tollin M., Olsson B., Svenberg T., Agerberth B.,
Gudmundsson G.H.;
Submitted (PRB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF484553; AAQ05977.1; -; mRNA.
GO; GO:0005576; C:extracellular region; IRA.
GO; GO:0005952; P:defense response; IRA.
GO; GO:0009613; P:response to pest, pathogen or parasite; IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibacterial peptide BMAP-14.
Pyrrolidone carboxylic acid.
Glycine amide (Potential).
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.6%; Score 454; DB 1; Length 165; 60.0%; Pred. No. 3.3e-35; ive 21; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 SPDISCDKDNKR--PALLGDFFRKSKEKIGKEFKRIVQRIKDFLR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21F14A0A68C6FBF0 CRC64;
                                                                 and testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                           EMBL; Y12729; CAA73261.1; -; Genomic_DNA.
EMBL; Y12729; CAA73261.1; JOINED; Genomic_DNA.
EMBL; P31.96; 1KW1.
SMR; P56425; 30-129.
INCETPO: IRROOL894; Cathelicidin.
Pfan; PFRO10206; Cathelicidin; 1.
Pfan; PF00666; Cathelicidin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential. Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18848 MW;
Lett. 417:311-315(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99; Conservative
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NCBI_TaxID=10116;
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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 PTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDIS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 LDPLPKGDKDSDTPKPVSFMVKETVCPRIMKQTPEQCDFKENGLVKQCVGTVILGPVKDH 119
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                                                                                                                                                                                                                                                                                                                                                                      5 RDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Bone marrow;
MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia, Eutheria, Laurasiatheria, Perissodactyla, Equidae, Equus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R Wovel catheliciding in horse leukocytes.";

R FEBS Lett. 457:459-464(1999).

R REMBL, AJ224927; CAA12226.1; -; mRNA.

R RSP; P32196; 1KWI.

R SPR; O62840; 30-130.

R GO; GO:0005576; C:extracellular region; IRA.

R GO; GO:0005613; P:edefense response; IRA.

R GO; GO:0009613; P:response to pest, pathogen or parasite; IRA.

R Ffam; PF00666; Cathelicidin; I.

R PROSITE; PS001989; Cathelicidin; I.

R PROSITE; PS001989; CATHELICIDINS 1; I.

R PROSITE; PS00946; CATHELICIDINS 1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 CDKDN-----KRFALLGDPPRKSKEKIGKEFKRIVQRIKDFLRNLVPRTE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E., Zanetti M.;
                                                                                                                                                                                                                                                                                                             7;
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                                                                                                                                                                                                                                                 DB 2; Length 171;
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56.2%; Pred. No. 6e-35;
ive 20; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                             48; Indels
                                                                                                                                                     NON TER 1 1 1 SEQUENCE 171 AA; 19320 MW; 7E8F3DA9DF10E839 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Myeloid cathelicidin 1 precursor.
Name=eCATH-1;
                                                                                                                                                                                                                                          51.6%; Score 453.5; DB 2
55.6%; Pred. No. 3.8e-35;
                                                                                                                                                                                                                                                                    55.6%; Preq. mismatches
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                            Pfam; PP00666; Cathelicidins; 1.
Probom; PD0018918; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
InterPro; IPR001894; Cathelicidin.
                                                                                                                                                                                                                                                                                                          95; Conservative
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O62840;
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156
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                                                                                                                                                                                                                                                                             Local Similarity
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062840 HOR
10 662840 AC
062844 AC
062844 DT 01-AU
DE MYSELS
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Tossi A., Scocchi M., Zanetti M., Storici P., Gennaro R.;
Tossi A., Scocchi M., Zanetti M., Storici P., Gennaro R.;
"PMAP-37, a novel antibacterial peptide from pig myeloid cells. cDNA cloning, chemical synthesia and activity.";
Eur. J. Blochem. 228:941-946 (1995).
-1- FUNCTION: Exerts antimicrobial activity against both Gram-positive and negative bacteria with minimal inhibitory concentrations ranging over 1-4 micro molar. Its activity appears to be mediated by its ability to damage bacterial membranes.
-1- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
13.58P-2005 (Rel. 48, Last amnotation update)
Antibacterial peptide PMAP-37 precursor (Myeloid antibacterial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
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                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Laurasiatheria, Cetartiodactyla, Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
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PANTHER; PTHRID206; Cathellicidin; 1.
Pfam; PP00666; Cathellicidin; 1.
ProDom; PD001838; Cathellicidin; 1.
PROSTIE; PS00946; CATHELICIDINS 1; 1.
PROSTIE; PS00947; CATHELICIDINS 2; 1.
Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
121 FDISCDKDN--KRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potential.
Antibacterial peptide PMAP-37.
Pyrrolidone carboxylic acid (By similarity).
                               120 FDVSCGEPQRVKRFG------MLAKSFLR------MRILLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.6%; Score 444.5; DB 1; Length 57.1%; Pred. No. 2.7e-34; Live 26; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE, AND SYNTHESIS OF 131-167
                                                                                                                                                                                           167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L39641; AAA63447.1; -; mRNA.
PIR; S68967; S68967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92; Conservative
                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
130
167
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124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P32196; 1KWI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85
107
167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131
                                                                                                                                                                                                                                                                                                                                                                                         Name=PMAP37;
                                                                                                                                                                                           \overline{PMP37} PIG P4993\overline{2};
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from sheep and goat laukocytes.;
Infect. Immun. 67:4106-4111(1999).
-!- FUNCTION: Bainds to the lipid a moiety of bacterial
lipopolysaccharides (LPS), a glycolipid present in the outer
membrane of all Gram-negative bacteria. Shows a potent
antimicrobial activity against Gram-negative bacteria B.coli,
S.typhimurium and P.aeruginosa. Less active against Gram-positive
bacteria S.aureus, L.monocytogenes and B.subtilis.
-!- DOMAIN: BACS sequence consists almost exclusively of X-P-P-Y
                                                                                                                                                                                                                                                                                                                                  "Purification and properties of proline-rich antimicrobial peptides
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                           NUCLECTIDE SEQUENCE OF 131-149 AND 151-153, AND PROTEIN SEQUENCE
                                                                                                                                                                                                                                                                       TISSUB=Bone marrow, and Leukocyte;
MEDLINE=99346202; PubMed=10417180;
Shamova O., Brogden K.A., Zhao C., Nguyen T., Kokryakov V.N.,
  120 LDINCDEIQSVGRFRRLRKKTRKRLKKIGKVLKWI 154
                                                                                                  (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 48, Last annotation update)
                                                                        176 AA
                                                                                                                                              Bactenecin 5 precursor (Bac5) (ChBac5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19846 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173
                                                                                                                                                                         Capra hircus (Goat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P32196; 1KWI.
SMR; P82018; 30-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                NCBI TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173
                                                                                                   30-MAY-2000
                                                                                                                                                                                                                                                                                                                      Lehrer R.I.;
                                                                        CAPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE
PROPEP
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPEP
                                           RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 LDQPPRADEDPGTPKPVSFTVKETVCPRPTWRPPELCDFKENGRVKQCVGTVTLNPSNDP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKTORDGHSIGRWSIVLLILIGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD 60
                                                                                                                                           01-OCT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Antibacterial peptide PMAP-36 precursor (Myeloid antibacterial peptide
                                                                                                                                                                                                                                                                                                                            MEDLINE=94123775; PubMed=8293820; DOI=10.1016/0014-5793(94)80214-9; Storici P., Scocchi M., Tosei A., Gennaro R., Zanetti M.; Storici P., Scocchi M., Tosei A., Gennaro R., Zanetti M.; Chemical synthesis and biological activity of a novel antibacterial peptide deduced from a pig myeloid cDNA."; FEBS Lett. 337:303-307(1994).

-I- FUNCTION: Exerts antimicrobial activity against both Gram-positive and negative bacteria. Its activity appears to be mediated by its ability to damage bacterial membranes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSEP; P32196; 1KWI.
SMR; P49931; 30-130.
InterPro; IPRO1894; Cathelicidin.
PANTHER; PTH710206; Cathelicidin; 1.
ProDom; P000666; Cathelicidins; 1.
ProDom; P0004838; Cathelicidin; 1.
PROSITE; P800946; CATHELICIDINS 1.
PROSITE; P800946; CATHELICIDINS 2; 1.
Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrrolidone carboxylic acid (By similarity).
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39; Indels
                94B13C69709DA64B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the cathelicidin family.
 121 FDISCDKDNK--RPALLGDFRKSKEKIGKEFKRIVQRIKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 PDISCDKDNK--RFALLGDFFRKSKEKIGKEFKRI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 3.3e-34;
18; Mismatches 39
                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE, AND SYNTHESIS OF 130-166.
                                                                                                   166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.5%; Score 443.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L29125; AAA31070.1; -; mRNA.
PIR; S41731; S41731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 AA; 18647 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95; Conservative
                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
                                                                                                                                                                                                                                                                                                                  TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                 Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>:</u>
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                                                                                                                                                                                                                                                                          NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
                                                                                                                                                                                      36).
Name=PMAP36;
                                                                                                                            01-OCT-1996
01-OCT-1996
                                                                                                  PMP36 PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
SEQUENCE
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                                                                                                            P49931;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR011894; Cathelicidin.
PANTHER; PTHR10206; Cathelicidin; 1.
PROSTER; PRO0666; Cathelicidin; 1.
PROSTE; P800946; CATHELICIDINS 1; 1.
PROSTE; P800946; CATHELICIDINS 1; 1.
AMIGHICH, ANTHELICIDINS 2; 1.
AMIGHICH, ANTHELICIDINS 2; 1.
PANTHER; P800947; CATHELICIDINS 2; 1.
PROSTER; P800947; CATHELICIDINS 2; 1.
PROSTER; P800947; CATHELICIDINS 2; 1.
PATCOLIGONE CATHELICIDINS 2; 1.
PATCOLIGONE CATHELICIDINS 2; 1.
PATCOLIGONE CATHELICIDINS 2; 1.
PATCOLIGONE CATHELICIDINS 2; 1.
POTCOLIGONE CATHELICIDINS 2; 1.
PROSTER; PROFESSIONE CATHELICIDINS 2; 1.
PROFESSIONE CATHELICIDINS 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proline amide (G-174 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bactenecin 5.
Removed in mature form.
Pyrrolidone carboxylic acid
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By similarity.
6FD7056C954E340A CRC64;
-!- PTM: Blastase is responsible for its maturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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Search completed: January 12, 2006, 21:50:32 Job time : 84.8044 secs
TISSUE=Liver:
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Best Local {
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            60 LDPAPNDEVDPGTRKPVSFTVKETVCPRTTQQPPERCDFKENGLVKQCVGTVTLDPSNDQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDPAPNDEVDPGTRKPVSFTVKETVCPRTTQQPPEECDFKENGLVKQCVGTVTLDPSNDQ 119
61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKXDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKTORDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                             "Purification and properties of proline-rich antimicrobial peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1,
                                                                                                                                                                                                                                                                                                                                                   Shamova O., Brogden K.A., Zhao C., Nguyen T., Kokryakov V.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 50.3%; Score 442.5; DB 2; Length Local Similarity 68.5%; Pred. No. 4.5e-34; Nes 87; Conservative 19; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y18873; CAC80206.1; -; mRNA.
SEQUENCE 176 AA; 19846 MW; 6FD7056C954E340A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P79360 SHEEP PRELIMINARY; PRT; 165 AA. P79360 01-MAY-1997 (TrEMBLrel. 03, Created) 01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-UTW-2003 (TrEMBLrel. 24, Last annotation update) Myeloid antimicrobial peptide.
                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                          176 AA
                                                                                                                                                                    Created)
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                         TISSUE=Bone marrow;
MEDLINE=99346202; Pubmed=10417180;
                                                                                                                                                                                                                                                                                                                                                                                          from sheep and goat leukocytes.";
Infect. Immun. 67:4106-4111(1999)
                                                                                                                                                                 13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Bac5 protein.
                                                                                                                                        Q4JFB9 CAPHI PRELIMINARY;
Q4JFB9;
                                                                                                                                                                                                                                  Capra hircus (Goat).
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FDINCNE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDISCDK 127
                                                 PDISCDK 127
                                                                |||:|::
|20 FDINCNE 126
                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                  Lehrer R.I.;
                                                                                                                                                                                                                       Name=bac5;
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P79360 SHE
D7936 AC
P7936
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MC
DN Mame
OC Mame
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OC PECON
RN NCBI
RN NCEL
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NUCLEOTIDE SEQUENCE

NCBI_TaxID=9940;

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61 LDPRPTMDG-DPDTPKPVSFTVKETVCPRTTQGSPEDCDFKKDGLVKRCMGTVTLNQARG 119
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MEDLINE=96440581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3; Mahoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Huttner K.M.; "Molecular analysis of the sheep cathelin family reveals a novel antimicrobial peptide.", FEBS Lett. 377:519-522(1995).
                                                                                                                                                                                                                            TISSUE-Liver;
A Huttner K.M., Mahoney M.M.;
Submitted (JUN-1956) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1956) to the EMBL/GenBank/DDBJ databases.
EMBL, U60597; AAB49712.1; -; Genomic_DNA.
R HSSP; P32196; ITWW.
R GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005576; C:extracellular region; IEA.
R GO; GO:0005613; P:response to pest, pathogen or parasite; IEA.
R GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
R PFOD; PRO0666; Cathelicidin.
R Pfam; PRO0666; Cathelicidin; 1.
R PRODITE; PS00946; CATHELICIDINS 1.
R PROSITE; PS00947; CATHELICIDINS 2; 1.
S ROGITE; PS00947; CATHELICIDINS 2; 1.
S ROGITE; PS00947; CATHELICIDINS 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.1%; Score 440; DB 2;
57.8%; Pred. No. 7.2e-34;
ive 22; Mismatches 42;
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                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Sequence 2, Appli
Sequence 2, Appli
Sequence 7862, Appli
Sequence 4, Appli
Sequence 33, Appli
Sequence 35, Appli
Sequence 35, Appli
Sequence 29, Appli
Sequence 29, Appli
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Sequence 4, Appli
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Sequence 6, Appli
Sequence 6, Appli
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                                                                      January 12, 2006, 21:45:19; Search time 26.3469 Seconds (without alignments) 533.455 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Ap
Sequence 8, Ap
Sequence 10, A
Sequence 4, Ap
Sequence 2, Ap
                                                                                                                       US-10-815-562-2
879
1 MKTQRDGHSLGRWSLVLLLL.....KRIVQRIKDFLRNLVPRTES 170
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-313-681A-2
US-09-322-911-2
US-09-312-911-2
US-09-513-995C-7862
US-08-313-681A-4
US-09-312-911-4
US-09-312-911-4
US-09-917-340-33
US-09-917-340-33
US-09-917-340-34
US-09-917-340-34
US-09-917-340-34
US-09-128-45-4
US-08-243-879A-42
US-08-243-878-6
US-09-128-345-6
US-09-128-345-8
US-09-128-345-10
US-09-385-328-4
US-09-385-328-4
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                              572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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47.3 149 2 US-09-385-328-8 46.9 160 2 US-09-317-340-28 37.9 78 2 US-09-317-340-28 37.0 96 1 US-09-317-340-28 37.0 96 1 US-09-313-995-4349 37.0 96 2 US-09-513-995-4349 37.0 96 2 US-09-513-995-4349 37.0 96 2 US-09-513-995-11-5 35.7 59 2 US-09-513-911-6 18.3 37 2 US-09-385-328-10 17.5 36 2 US-09-385-328-11 15.1 27 2 US-09-385-328-11 15.1 27 2 US-09-385-328-11 15.3 37 2 US-09-36-202-8 13.3 37 2 US-09-376-202-8 13.4 27 2 US-09-276-202-8 13.3 27 2 US-09-276-202-9 13.4 27 2 US-09-276-202-1 13.3 27 2 US-09-276-202-1 13.4 27 2 US-09-276-202-1 13.5 27 2 US-09-276-202-1 13.6 2 US-09-276-202-1 13.8 27 2 US-09-276-202-1 14.1 27 2 US-09-276-202-1 15.1 BATCOMPATION 1 Hoppolysaccharide Binding and BOTENTICK, James W. Mishimasa NEMTION: Human Cationic Proteins Having VENTION: Human Cationic Proteins Having USA, DOOR MARKET Plaza, Steuart Tower, Suite 205 11.2 2 US-09-276-202-1 12.9 23 2 US-09-276-202-1 13.3 27 2 US-09-276-202-1 14.1 2.5 2 US-09-276-202-1 15.1 US-085/MS-DOS 16.1 US-085/MS-DOS 16.1 US-085/MS-DOS 17.1 US-085/MS-DOS 18.1 US-085/MS-DOS 18.1 US-085/MS-DOS 18.1 US-085/MS-DOS 18.1 US-085/	e 36, Appli e 26, Appli e 27, Appli e 5, Appli e 7, Appli e 10, Appli e 6, Appli e 6, Appli e 7, Appli e 10, Appli e 10, Appli e 2, Appli e 10, Appli e 10, Appli e 10, Appli	ant Activit	Gaps 0;
47.3 149 2 US-09-385-328-8 46.9 160 2 US-09-917-340-36 37.0 96 2 US-09-917-340-38 37.0 96 2 US-09-917-340-38 37.0 96 2 US-09-913-881A-5 35.7 59 2 US-09-313-881A-5 37.1 US-08-313-881A-6 18.3 37 1 US-08-313-881A-6 18.3 37 1 US-09-318-328-11 18.1 37 2 US-09-376-302-8 13.3 27 2 US-09-376-302-8 13.3 27 2 US-09-376-302-8 13.3 27 2 US-09-376-202-1 13.4 27 2 US-09-376-202-1 13.5 27 2 US-09-376-202-1 13.5 27 2 US-09-376-202-1 13.6 ENTIREMENTS ALIGNMENTS ALIGNMENT	equence equenc	Anti-Coagulant	170,
47.3 1 46.9 1 1 46.9 1 1 37.0	2 US-09-318-328-8 2 US-09-917-340-36 2 US-09-917-340-28 2 US-09-913-9990-434 US-08-313-681A-5 2 US-09-32-911-5 2 US-09-32-911-6 2 US-09-385-328-17 US-08-313-681A-6 1 US-08-313-681A-6 2 US-09-35-32-911-6 2 US-09-276-202-8 2 US-09-276-202-8	ALIGNMENTS 13681A W. Sa Cationic Proteins Ha Lysaccharide Binding Townsend Khourie and Steuart Tower, Sui Steuart Tower, Sui B/313,681A 15325-9-1 ON:	.0%; Score 879; DB 1; L .0%; Pred. No. 1.1e-95; 0; Mismatches 0;
	415.5 415.5 410.13 410.13 410.13 410.13 41	SEULT 1 S-08-313-681A-2 Sequence 2, Application Patent No. 5618675 GENERAL INFORMATION: APPLICANT: Hirtat, MIGHT, SAPLICANT: HIRTAT, MIGHT, SAPLICANT: HIRTAT, MITTLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS ADDRESSER: TOWNERS ADDRESSER: TOWNERS ADDRESSER: TOWNERS ADDRESSER: TOWNERS ADDRESSER: TOWNERS ADDRESSER: TOWNERS ANDRESSER: TOWNERS CONTRY: USA ZIP: 94105 COMPUTER READABLE FOR MEDIUM TYPE: Floppe COMPUTER: LUB PC COMPUTER: BAPLICATION DAPLICATION NUMBER: FILING DATE: CLASSIFICATION NUMBER: FILING DATE: CLASSIFICATION NUMBER: REFERENCE/DOCKET UNTELEPHONE: 415-326-2 INFORMATION FOR SEQ ID SEQUENCE CHARACTERIST TELEPHONE: 415-326-2 INFORMATION FOR SEQ ID SEGUENCE CHARACTERIST TELEPHONE: 415-326-2 INFORMATION FOR SEQ ID SEGUENCE CHARACTERIST TYPE: amino acid STRANDEDNESS: sing TOPPOLOCY: linear MOLECULE TYPE: prote	vat

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1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                         Sequence 32, Application US/0991340

Fatent No. 6696238

GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: Machulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2000-07-28
FRIOR FILING DATE: 2000-07-28
FRIOR FILING DATE: 2000-11-17
FRIOR APPLICATION NUMBER: 60/249,602
FRIOR APPLICATION NUMBER: 60/249,602
FRIOR APPLICATION NUMBER: 60/249,602
FRIOR APPLICATION NUMBER: 60/29,602
FRIOR APPLICATION NUMBER: 60/249,602
FRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PATENTING DATE: 2011-05
SEQ ID NO 3:
LEBNGTH: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-09-917-340-32
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US-09-513-999C-7862
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Patent No. 6103888
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Hirata, Mishimasa
APPLICANT: Hirata, Mishimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESCONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: TWO Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                            61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVRRCMGTVTLNQARGS 120
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100.0%; Score 879; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.1e-95;
Matches 170; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
GOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/322,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 17, 1993
PRIOR APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION NUMBER: 08/313,681
FILING DATE: July 15, 1993
PRIOR APPLICATION NUMBER: 08/313,681
FILING DATE: SEPTEMBER 1, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A. 15325-00092(
TELEFAX: A15-326-2400
TELEFAX: A15-326-2400
TELEFAX: A15-326-2402
TELEFAX: LANGER SEQ ID NO: 2:
SEGUENCE FRRACTERISTICS:
LENGTH: 170 amino acids
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
COUNTRY: USA
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; Sequence 7862, Application US/09513999C
; Reinstan Information
; APPLICANT: Duclert, A.
; APPLICANT: Duclert, A.
; APPLICANT: Duclert, A.
; TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT PILLING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; FRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
                                                                                                      61 LDPRPTWDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Larrick, Susan C.
APPLICANT: Hizata, Mishimssa
APPLICANT: Hizata, Mishimssa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                  61 LDPRPTMDGDPDTPKPVSFTVKBTVCPRTTQQSPBDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                           60 MDPQQLEDAKPYTPQPVSFTVKETECPRTTWKLPEQCDFKEDGLVKRCVGTVTRYQAWDS 119
                                                                                1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
       Gape
                                                                                                                                                                                                                                                                            121 FDISCDK--DNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTE 169
       3,
     44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSER: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
     26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/313,681
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 35,136
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09322911
Patent No. 6103888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 171 amino acids TYPE: amino acid
     98; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    California
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     Matches
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Sequence 4, Application US/08313681A

Patent No. 5618675

GENERAL INFORMATION:
APPLICANT: Wright, James W.
APPLICANT: Wright, Suan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                             4 MKTQRDGHSLGRWSLVLLLIGLVWPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 63
                                                                                                                                                                                                                                                                                                                                                                    1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                       Length 152
                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPER Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
                                                                                                                                                                                                                                                                 86.6%; Score 761; DB 2;
98.6%; Pred. No. 8.2e-82;
iive 1; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 PDISCDKDNKRFALLGDFFRKSKEKIGK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:

"NAME/KEY: SIGNAL

"CCATION: -33...1

"OTHER INFORMATION: SEQ LLLGLVMPLAIIA/QV
US-09-513-999C-7862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REPRENCE/POCKET NUMBER: 1532
TELECOMMUNEATION:
TELEPHONE: 415-326-2400
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57.3%;
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.69
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-313-681A-4
                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Best Local Similarity
SEQ ID NO 7862
LENGTH: 152
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US-08-313-681A-4
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RESULT 9
US-09-917-340-34
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                                                                                                                                                               LENGTH: 156
                                                                                                                                          SEQ ID NO 35
                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                      60 MDPQQLEDAKPYTPQPVSFTVKETECPRTTWKLPEQCDFKEDGLVKRCVGTVTRYQAMD$ 119
                                                                                                                                                                 61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDPRPTMDGDPDTPKPVSFTVKBTVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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                                                                                                                         23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 METQRNTRCLGRWSPLLLLLGLVIPPA-TTQALSYKBAVLRAVDGLNQRSSDENLYRLLE 59
                                                                                 1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD
                                                                                                      Gaps
                                                                                                                                                                                                                                              121 PDISCDK--DNKRPALLGDPPRKSKEKIGKEFKRIVQRIKDFLRNLVPRTE 169
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    Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 PDISCDKDN--KRFALLGDFFRKSKEKIGKEFK-----RIVORIK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 53.0%; Score 465.5; DB 2; Length 1
1 Similarity 57.3%; Pred. No. 8e-47;
98; Conservative 26; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                            US-09-917-340-39

US-09-917-340-39

Patent No. 6696236

GENERAL INFORMATION:

APPLICANT: Murphy, Christopher J.

APPLICANT: McAnulty, Jonathan F.

APPLICANT: McAnulty, Jonathan F.

APPLICANT: Reid, Ted W.

TILLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468

CURRENT APPLICATION NUMBER: US/09/917,340

CURRENT FILING DATE: 2001-07-29

PRIOR FILING DATE: 2000-07-29

PRIOR FILING DATE: 2000-07-29

PRIOR FILING DATE: 2000-01-17

PRIOR PRILING DATE: 2000-01-17

PRIOR PRILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PATENT ON UNBER: 60/290,932

NUMBER OF SEQ ID NOS: 96

SOFTWARE: 170
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Patent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: Marphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REPERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
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Best Local Similarity 57.24
Matches 95; Conservative
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; ORGANISM: Equus caballus
US-09-917-340-33
Query Match
Best Local Similarity
Matches 98; Conserve
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61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.3%; Score 451; DB 2; Length 156; 56.2%; Pred. No. 3.6e-45; Live 20; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JUS-09-91/1-340-340

JUS-09-91/1-340-340

JUS-09-91/1-340-340

JUS-09-91/1-340-340

JUS-09-91/1-340-340

JUS-09-91/1-340-340

JUS-09-91/1-340

PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Equus asinus US-09-917-340-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 85; Conserva
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120 NFDITC 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 95; Conserv
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GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: ROKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTECTINE
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/08499523
; Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 2000
TELECOMMUNICATION:
                 TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
(202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
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                                                                                                                                                                                                                                                                     83; Conservative
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Best Local Similarity 65.4
Matches 83; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 147 amino acids
                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
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MOLECULE TYPE: protein
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Best Local Similarity
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  TELEPHONE:
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US-08-499-523-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.6%; Score 427.5; DB 2; Length 155; 66.7%; Pred. No. 2.1e-42; tive 18; Mismatches 23; Indels 1.
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Sequence 38, Application US/08243879A

Patent No. 5708145

GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORRSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 2006-1812
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
                              US-09-917-340-29

1 Sequence 29 Application US/09917340

1 Sequence 29 Application US/09917340

2 Sequence 29 Application US/09917340

3 GENERAL INVORMATION:

APPLICANT: MacAnily, Jonathan F.

APPLICANT: Reid, Ted W.

TITLE OF INVENTION: Transplant Media

FILE REPERENCE: TPLANT-06468

CURRENT APPLICATION NUMBER: US/09/917,340

CURRENT FILING DATE: 2001-07-29

PRIOR APPLICATION NUMBER: 60/221,632

PRIOR PILING DATE: 2000-11-17

PRIOR FILING DATE: 2000-11-17

PRIOR FILING DATE: 2000-11-17

PRIOR FILING DATE: 2000-11-17

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PATCH IN VET: 2.0

SEMENTH: 155
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ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.74
Matches 84; Conservative
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US-09-917-340-29
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FDITCN 125
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61 LOPRPTMDGDPDTPKPVSFTVKRTVCPRTTQQSPRDCDFKKDGLVKRCMGTVTLNQARGS 120
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                                                                                                                                          1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
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47.6%; Score 418.5; DB 1; Length 147; 65.4%; Pred. No. 2.3e-41;
                                                     19; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
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US-08-243-879A-36
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                                                                                                                                                                 61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQGSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/128,345

FILING DATE: 03-AUG-1998

CLASSIPICATION: 514

ATTORNEY APAGENT INFORMATION:

NAME: COTIZZI, Laura, A.

REGISTRATION NUMBER: 8067-0054-999

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEPAK: (212) 869-9741

TELEX: (6141 PENNIE

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 147 amino acids

TYPE: amino acids

TYPE: ALL ATTORNEY ACIDS

TOTAL ATTORNEY ACIDS

TOTAL ACIDS

TOTAL ACIDS

TELEPAK: (112) 869-9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 147 amino acids

TYPE: ALL ATTORNEY ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09128345; Patent No. 6159936; Batent No. 6159936; GENERAL INFORMATION; APPLICANT: LEHERR, APPLICANT: HARWIG, SYLVIA S.L. APPLICANT: KOKRYAKOV, VLADIMIR N. TITLE OF INVENTION: PROTEGRINS NUMBER OF SEQUENCES: 76 CORRESPONDENCE ADDRESSE: ADDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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120 LDITCNE 126
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61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40, Application US/08243879A; Patent No. 5708145; GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARNIG, SYLVIA S.L.
TITLE OF INVENTION: A NEW PROTECRIN NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS;
Sequence 36, Application US/08243879A
Patent No. 5708145
GENERAL INFORMATION:
APPLICANT: HERRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
ITILE OF INVENTION: A NEW PROFECTION NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER:
ADDRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 149 amino acids TYPE: amino acid
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COMPUTER READABLE FORM:
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Query Match 47.6%; Score 418.5; DB 1; Length 149; Best Local Similarity 65.4%; Pred. No. 2.3e-41; Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Pc-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIFCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MURABAHIGA: KATE H.
SEGISTRAATION NUMBER: 2000-0540.22
TELECOMMUNICATION INFORMATION:
TTELES 90-4030
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: maino acide
TYPE: TOPOLOGY: linear
MOLECULE TYPE: protein
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Search completed: January 12, 2006, 21:51:59 Job time : 26.3469 secs

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1204, App
11204, App
133, Appl
133, Appl
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35, Appl
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35, Appl
35, Appl
36, Appl
37, Appl
37, Appl
37, Appl
34, Appl
                                                    January 12, 2006, 21:45:40 ; Search time 70.2583 Seconds (without alignments) 1010.998 Million cell updates/sec
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Sequence 32,
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Sequence 3
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'Ggn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

'Ggn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-893-485-51
US-10-844-837-32
US-10-77-683-4
US-10-657-851-32
US-10-657-851-32
US-10-287-436A-1204
US-10-344-709C-7
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US-10-344-709C-7
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US-09-917-340-29
US-10-344-709C-8
US-10-844-837-29
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                                                                                                                                                           1867569 seqs, 417829326 residues
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Maximum Match 100%
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                                                        Run on:
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Sequence 51, Application US/10603566

Sequence 51, Application US/10603566

Dublication No. US20040086966A1

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Vandenbogaerde, Ann
APPLICANT:
Vandenbogaerde, Ann
APPLICANT:
Parmentier, Marc
TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
FILE REPERENCE: 9409/2212

CURRENT FILING DATE: 2003-06-25

PRIOR PILING DATE: 2001-07-09

PRIOR PILING DATE: 2001-07-13

PRIOR PILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-23

NUMBER OF SEQ ID NOS: 91

SOUTHWARE: Patentin version 3.2
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24, Appli
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US-10-657-851-29
US-09-539-443-4
US-09-539-443-6
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US-10-893-485-51
i. Sequence 51, Application US/10893485
i. Publication No. US20050155090A1
i. GENERAL INFORMATION:
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; LENGTH: 170
; TYPE: PRT
: ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-844-837-32
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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             APPLICANT: Communi, David
APPLICANT: Communi, David
APPLICANT: Vandenbogaerde, Ann
APPLICANT: Dethew, Michel
APPLICANT: Parmentier, Marc
ITILE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
FILE REFERENCE: 3409/24045.
FILE REFERENCE: 3409/24045.
CURRENT APPLICATION NUMBER: US 60/303,858
PRIOR APPLICATION NUMBER: US 60/303,656
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2003-06-25
PRIOR PLING DATE: 2001-07-13
PRIOR PELING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
SOFTWARE: PATENTING DATE: 2001-07-23
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99.4%; Pred. No. 5.9e-87;
tive 1; Mismatches 0; Indels
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Fatent No. US20020090369A1
GREREAL INFORMATION
FAPPLICANT: Wurphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
FILE REPERBNG: TPLANT-06468
CURRENT FILING DATE: 2001-07-29
FRIOR APPLICATION NUMBER: 60/221,632
FRIOR PILING DATE: 2000-07-28
FRIOR PILING DATE: 2000-11-17
FRIOR PILING DATE: 2000-11-17
FRIOR PILING DATE: 2001-11-17
FRIOR PILING DATE: 2001-05-15
FRIOR PILING DATE: 2001-05-15
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FRIOR FILING DATE: 2001-05-15
Wittamer, Valerie
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Matches 169; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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; Publication No. US20050032117A1
; Publication No. US20050032117A1
; GENERAL INPORMATION:
; APPLICANT: Richard B. Moss
; APPLICANT: Akitoshi Ishizaka
; APPLICANT: Teruo Kirikae
; TILE COF INVENTION: Method for Assessment of Cystic Lung Fibrosis
; FILE REFERRING: Q74236
; CURRENT PRILICATION NUMBER: US/10/777,683
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/447,310
; PRIOR PILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
                                                                                                                                                                                                                                            121 FDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
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Sequence 32, Application US/10844837
Publication No. US20050014932A1
GENERAL INFORMATION:
APPLICANT: Imboden, Michael
APPLICANT: Homan, Jane
TITLE OF INVENTION: Targeted Biocides
FILE REFERENCE: IOGEN-09014
CURRENT APPLICATION WUMBER: US/10/844,837
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin version 3.2
SEQ ID NO 32
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SEQ ID NO 32
LENGTH: 170
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Publication No. US20050079578A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Centanni, John M.
APPLICANT: Allen-Hoffmann, Lynn
TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
CURRENT APPLICATION NUMBER: US/10/909,119
CURRENT PILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.2
SEQ ID NO 47.
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   1; Mismatches
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Publication No. US20050089836A1
GENERAL INPORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: Medanity, Jonathan F.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT FILING DATE: 2003-09-09
FRIOR PILING DATE: 2001-09-09
PRIOR PRILING DATE: 2001-07-29
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-15-8
PRIOR FILING DATE: 2000-15-8
PRIOR FILING DATE: 2000-15-8
PRIOR FILING DATE: 2000-15-8
PRIOR FILING DATE: 2000-16-15-8
PRIOR FILING DATE: 2000-16-15-8
PRIOR FILING DATE: 2000-15-15-8
PRIOR FILING DATE: 2000-15-1
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   169; Conservative
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ORGANISM: Homo sapiens
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US-10-909-119-47
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US-10-657-851-32
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LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPBDCDFKWDGLVKRCMGTVTLNQARGS 120
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                                                                                                             Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAPLICATION OF THE PROPERTY MEDICAL CENTER TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: RHEHOMATOID ARTHRITIS

FILE REPERENCE: 10872.514696

CURRENT APPLICATION NUMBER: US/10/287,436A

PRIOR APPLICATION NUMBER: US 60/336,220

PRIOR APPLICATION NUMBER: US 60/336,220
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Publication No. US20050202421A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: RHEUMATOID ARTHRITIS
FILE REFERENCE: 10872.514656
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/336,220
                                                                                                        Score 874; DB 5;
Pred. No. 5.9e-87;
1; Mismatches 0;
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 513
LENGTH: 170
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Sequence 513, Application US/10287436A
Publication No. US20050202421A1
GENERAL INFORMATION:
                                                                                                             99.4%;
                                                                                                             Query Match
Best Local Similarity 99.4<sup>1</sup>
Matches 169; Conservative
TYPE: PRT
CORGANISM: Homo sapiens
US-10-657-851-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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US-10-287-436A-1204
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TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof FILE OF INVENTION: 3000 CURRENT APPLICATION NUMBER: US/10/344,709C CURRENT FILING DATE: 2003-02-14 PRIOR FILING DATE: 2001-08-17 PRIOR FILING DATE: 2001-08-17 PRIOR FILING DATE: 2000-08-17 PRIOR FILING DATE: 2000-08-17 SEQ ID NOS: 23 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-10-344-709C-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FARENTAL INFORMATION:
APPLICANT: MacAulty, Christopher J.
APPLICANT: MacAulty, Christopher J.
APPLICANT: MacAulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT PILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR PILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR PILING DATE: 2001-11-7
PRIOR FILING DATE: 2001-11-7
PRIOR FILING DATE: 2001-07-28
PRIOR FILING DATE: 2001-07-28
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2011-05-15
PRIOR FILING DATE: 2011-05-15
PRIOR FILING DATE: 2011-05-15
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                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
       APPLICANT: JORG FRITZ ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Equus caballus
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Best Local S:
Matches 95;
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Bublication No. US20040170642A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof

FILE REFERENCE: SONN:0300S

CURRENT APPLICATION NUMBER: US/10/344,709C

CURRENT APPLICATION NUMBER: PCT/EP01/09529

PRIOR APPLICATION NUMBER: PCT/EP01/09529

PRIOR PILING DATE: 2000-08-17

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver: 2.1

SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKTQRNGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
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                                                                                                                                                                                                                                    Length 170;
                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                               Query Match
99.4%; Score 874; DB 5;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 1446
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1204
LENGTH: 170
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ORGANISM: Artificial Sequence
                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                US-10-287-436A-1204
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60 LDPLPKGDKDSDTPKPVSFMVKETVCPRIMKQTPEQCDFKENGLVKQCVGTVILDPVKDY 119
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                                                121 PDISCDKDN--KRPALLGDFPRKSKEKIGKEPK-----RIVQRIK 158
                                                                        121 PDISCDKDN--KRFALLGDFFRKSKBKIGKEFK-----RIVQRIK 158
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                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Teal, Ted W.
TILLS OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/10/657,851
CURRENT APPLICATION NUMBER: US/09/917,340
PRIOR FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-11-17
SOFTWARE: PARENT PARENT PARENT PARENT FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 33
LENGTH: 170
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Job time : 71.2583 secs
                                                                                                                                                                                                          Sequence 33, Application US/10657851; Publication No. US20050089836A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Equus caballus
US-10-657-851-33
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Sequence 48, Application US/10909119
Publication No. US20050079578A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Centanni, John M.
APPLICANT: Allen-Hoffmann, Lyun
TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
FILE REFERENCE: STRATA-09123
CURRENT APPLICATION WUMBER: US/10/909,119
CURRENT APPLICATION WUMBER: US/10/909,119
CURRENT PILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.2.
SEQ ID NO 48
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  LDPLPKGDKDSDTPKPVSFMVKETVCPRIMKQTPEQCDFKENGLVKQCVGTVILDPVKDY 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 170;
                                                  FDISCDKDN--KRFALLGDFFRKSKEKIGKEFK-----RIVQRIK 158
                                                                             121 FDISCDKDN--KRFALLGDFFRKSKEKIGKEFK-----RIVQRIK 158
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                                                                                                                                                                                                   Sequence 33, Application US/10844837
Publication No. US20050014932A1
GENERAL INFORMATION:
APPLICANT: Imboden, Michael
APPLICANT: Bremel, Mobert D.
APPLICANT: Bremel, Targeted Biocides
FILE REFERENCE: IOGEN-09014
CURRENT APPLICATION TARGETED
CURRENT APPLICATION UNDERS: US/10/844,837
CURRENT PILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin version 3.2
LENGTH: 170
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Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Equus caballus
US-10-844-837-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Equus caballus
                                                                                                                                                                                     US-10-844-837-33
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Sequence 1013, Ap Sequence 8036, Ap Sequence 33, Appl Sequence 1283, Appl Sequence 1016, Ap Sequence 1016, Ap Sequence 1076, Ap Sequence 159, Appl Sequence 196, Appl Sequence 196, Appl Sequence 196, Appl Sequence 25, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 26, Appl Sequence 27, Appl Sequence 20, Appl

OM protein

Run on:

Sequence:

Title:

Minimum DB Maximum DB

Database

Searched:

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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 37
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APPLICANT: Rajeev, Kallanthottathil G.
TITLE OF INVENTION: IRRA AGENTS WITH BIOCLEAVABLE TETHERS
FILE REPERRYCE: 1414-09001
CURRENT FILING DATE: 2004-11-09
PRIOR PLICATION NUMBER: US/10/985,426
CURRENT FILING DATE: 2004-01-09
PRIOR PLICATION NUMBER: US/0916,185
PRIOR PLICATION NUMBER: PCT/US2004/011829
PRIOR PLICATION NUMBER: US 60/465,665
PRIOR PLICATION NUMBER: US 60/465,665
PRIOR PLICATION NUMBER: US 60/465,665
PRIOR PLICATION NUMBER: US 60/465,612
PRIOR PLICATION NUMBER: US 60/465,802
PRIOR PLICATION NUMBER: US 60/493,986
PRIOR PLICATION NUMBER: US 60/495,97
PRIOR PLICATION NUMBER: US 60/494,597
PRIOR PLICATION NUMBER: US 60/503,414
PRIOR PLICATION NUMBER: US 60/506,341
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21.0%; Score 185; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.2e-14;
Matches 37; Conservative 0; Mismatches 0; Indels
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COTHER INFORMATION: Exemplary Cell Permeation Peptides
US-10-985-426-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 LLGDPPRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
US-10-821-234-1013

US-10-467-667-8036

US-11-186-284-33

US-11-186-284-33

US-10-995-561-1016

US-10-995-561-1016

US-11-033-365-159

US-11-033-365-196

US-11-033-365-196

US-11-033-365-197

US-11-033-365-196

US-11-00-184-468-25

US-10-954-468-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 9, Application US/10985426; Publication No. US20050256069A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
        US-10-985-426-9
      60.55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 406, App
Sequence 2104, Ap
Sequence 20, Appl
Sequence 6, Appli
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1990, Ap
134, App
1002, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Appli
                                                                                                                                                     January 12, 2006, 21:48:15; Search time 7.52768 Seconds (without alignments) 213.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                      1 MKTQRDGHSLGRWSLVLLLL.....KRIVQRIKDFLRNLVPRTES 170
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1: /cgn2_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USIO_NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USIO_NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USII_NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USII_NEW PUB.pep:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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US-10-793-626-406
US-10-793-626-2104
US-10-131-0266-2104
US-10-933-025-6
US-10-933-025-6
US-10-933-025-6
US-11-196-475-68
US-11-192-967-2
US-11-193-715-2
US-11-193-715-8
US-11-012-365-198
US-11-012-365-200
US-11-074-176-254
US-11-074-176-362
US-11-074-176-362
US-11-074-176-362
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US-11-074-176-362
US-11-074-176-363
US-11-074-176-363
US-11-074-176-363
US-11-074-176-363
US-11-074-176-363
US-11-074-176-363
US-11-070-463-347
US-11-100-183-17
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US-11-074-176-134
US-10-453-372-1002
US-11-174-150-42
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                                                                                                                                                                                                                                                                                                                                                                                               67062 seqs, 9454214 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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879
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1061
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Ç. Result

LLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 37

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PRIOR APPLICATION NUMBER: 60/049911
PRIOR PILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR PILING DATE: 1997-08-26
PRIOR PPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stewart, Timothy A.
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Filvaroff, Ellen
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Best Local Similarity
Matches 47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :|::||::: || | :|::: || 32 WHFILVILGIILLTSIITVVSTILISHQKS-----GLN-KEQRANLKKIEYVYQTLNKD 84
                                                                                                                                        APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILLE REFERENCE: PU348002
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE PACENTIN Ver: 2.1
SEQ IP NO 406
LENGTH: 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2104, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2104
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US-10-793-626-406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.7%; Score 76.5; DB 6; Length 491;
21.3%; Pred. No. 0.91;
tive 30; Mismatches 65; Indels 2
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                                                          US-10-793-626-406

"Sequence 406, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 33; Conserva
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63 PRPIMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGSFD 122
                                                                          ---IG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TORDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLDLD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330RIG128
CURRENT APPLICATION NUMBER: US/10/131,826A
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PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059352
PRIOR APPLICATION NUMBER: 60/059352
PRIOR PILING DATE: 1997-09-19
                                                                          85 YYKKQSSDKLİQSAIDGMVKELKDPYSEYMTAEBIKQFNEGVSGDFVG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.0%; Score 70.5; DB 6; Length 867; 20.4%; Pred. No. 9.1;
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                                                                                                                                                                                                                      135 AEMQKKNEQISVTSPMKDSPAEKAGIQPKDIVTQV 169
                                                                                                                                                        123 ISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION:
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                                  365 LAPTILDIAGLDIPADMDGKSILKLLDTERPVNRFHLKKKKMRVWRDSFLVERGKLLHKRD 424
                                                                               ---ETVCPRTTQ--QSPEDCDFXKDGLVKRCMGTVT 113
                                                                                                                  425 NDKVDAQEENFLPKYQRVKDLCQRABYQTACEQLGQKWQCVEDATGKLK--LHKCKGPMR 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ETVCPRTTQ--QSPEDCDFKKDGLVKRCMGTVT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 NDKVDAQEENFLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLK--LHKCKGPMR 482
  ---SFTVK----- 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                               114 INQAR-----GSFDISCDKDNKRFALLGDFFRKSKEKIGKEFK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 LNQAR------GSFDISCDKDNKRFALLGDFFRKSKEKIGKEFK 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.0%; Score 70.5; DB 6; Length 870; Best Local Similarity 20.4%; Pred. No. 9.1; Matches 47; Conservative 27; Mismatches 59; Indels 9
                                                                                                                                                                                                                                                                                    Sequence 6, Application US/10933025
Publication No. US20050265987A1
GENERAL INFORMATION:
APPLICANT: ROSMATION:
APPLICANT: HEMMERICH, STEFAN
APPLICANT: HEMMERICH, STEFAN
APPLICANT: TOMITA, MEGUMI
ITILE OF INVENTION: SUlfortansferases and methods of use;
TITLE OF INVENTION: LABCON
CURRENT PELICATION WHORE: US/10/933,025
CURRENT FILING DATE: 20004-09-01
PRIOR APPLICATION NUMBER: 10/025,966
PRIOR PELING DATE: 20001-12-27
PRIOR PELING DATE: 20001-09-02
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
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; Sequence 15, Application US/10933025
; Publication No. US2050265987A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEVEN
; APPLICANT: TOWAITA, MEGUMI
; TITLE OF INVENTION: Sulfotransferases and methods of use; FILE REFERENCE: UCAL-230CON
; CURRENT APPLICATION NUMBER: US/10/933,025
63 PRPT----DIPKPV-
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ORGANISM: Homo sapiens
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LENGTH: 870
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Sequence 1409, Application US/10821234

Sequence 1409, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Tuan

APPLICANT: Adarmani, Susan

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT PILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR PILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SEQ ID NO 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ETVCPRTTQ--QSPEDCDFKKDGLVKRCMGTVT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| | : | | : :| | : | | 425 NDKVDAQBENFLPRYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLK--LHKCKGPMR 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLDLD 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 PRPT-----SPTVK------SPTVK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 INQAR------GSPDISCDKDNKRPALLGDPFRKSKEKIGKEFK 151
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
8.0%; Score 70.5; DB 6; Length 870;
Best Local Similarity 20.4%; Pred. No. 9.1;
Matches 47; Conservative 27; Mismatches 59; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6; Length 645;
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Best Local Similarity 24.0%; Pred. No. 6.8;
Matches 36; Conservative 22; Mismatches
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CURRENT FILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: 10/025,966
PRIOR FILING DATE: 2001-12-21
PRIOR PILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/268,577
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2001-09-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PRESEQ for Windows Version 4.0
SOFTWARE: 970
                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-933-025-15
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; ORGANISM: Homo sapiens
US-10-821-234-1409
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38;

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73 TPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKRF 132
                                                                                                                                                                                                                                                                                                  200 TSTKKSKDTKODANSTTQSQTSITTDFADGG-----NNITLSNTNGKVEVT-----P 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 -----IDDNP----PILQVVSACVIPEHGEARLTDCVYQVSDRDGEISTRFMTPRVDS 214
                                                                                                                                                         13 WSLVLLLIGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPD
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; Bublication No. US2005026287A1
; Bublication No. US2005026287A1
; GENERAL INFORMATION:
; APPLICANT: Riamagan, Ronald D.
; APPLICANT: Mathis, John P.
; APPLICANT: Meyer, Terry B.
; TITLE OF INVENTION: Lepidopteran Insects and Methods of Use FILE OF INVENTION: Lepidopteran Insects and Methods of Use PILE REFERENCE: 35718/204664
; CURRENT APPLICATION NUMBER: US/11/192,967
; CURRENT APPLICATION NUMBER: US/09/715,909
; PRIOR PILING DATE: 2000-11-17
; PRIOR PILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SRO ID NO 2.
; TRACELL 17
                                                                                                                                                                                                             165 WALILLIL-----LALTIISYVGYVV----YNOLQTDSNKTEL----
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APPLICANT: Mathis, John P.
APPLICANT: Mathis, John P.
TITLE OF INVENTION: Novel Bt Toxin Receptors From
TITLE OF INVENTION: Lepidopteran Insects and Methods of Use
FILE REFERENCE: 35718/204664
CURRENT APPLICATION NUMBER: US/11/193,715
                                                 7.2%; Score 63; DB 7; Length 325; 22.4%; Pred. No. 15; attive 15; Mismatches 44; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.2%; Score 63; DB 7; 18est Local Similarity 19.7%; Pred. No. 1.6e+02; Matches 28; Conservative 24; Mismatches 52
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215 SRAA-----DESIFYMVGEY 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Ostrinia nubilalis
US-11-192-967-2
                                                                                                        Conservative
                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          247 TLTGD 251
  US-11-052-554A-356
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REPERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 TSDENQKREIEKQ-----IBIKKSDEELLKSKDPKALDLNGDLNSKVSSKEKIKGKEGE 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 EDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKRFALLGDFFRK--SKEKI-GKEFK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 KEAVLRAIDGINORSSDANLYRLLDLDPRPTMDGDPDTPK-PVSFTVKETVCPRTTQQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 7.3%; Score 64.5; DB 7; Length 693;
1 Similarity 27.1%; Pred. No. 30;
36; Conservative 21; Mismatches 53; Indels 23; Gaps
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Burgdorferi
TITLE OF INVENTION: Burgdorferi
TITLE OF INVENTION: Burgdorferi
FILE REPERBRENCE: 2631.1001-011
FILE REPERBRENCE: 2051.001-011
CURRENT APPLICATION NUMBER: US 08/148,191
PRIOR APPLICATION NUMBER: US 08/148,191
PRIOR APPLICATION NUMBER: US 08/25,836
PRIOR FILING DATE: 1993-11-01
PRIOR FILING DATE: 1994-04-29
PRIOR PLILING DATE: 2000-09-19
PRIOR PLILING DATE: 2000-09-19
PRIOR PLILING DATE: 2000-09-19
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 213
SOFTWARE: PABLEEC for Windows Version 4.0
  81 TVLLEFYAPWCGHCKQFAPEYEKIANILKD 110
                                                                                                                                                                                                          APPLICANT: Dattwyler, Raymond J.
APPLICANT: Gomes Solecki, Maria J. C.
APPLICANT: Luft, Benjamin J.
APPLICANT: Dunn, John J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 356, Application US/11052554A Publication No. US20050288866A1 GENERAL INFORMATION:
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                                                                                                                                Sequence 68, Application US/11196475
Publication No. US20050271682A1
GENERAL INFORMATION:
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US-11-196-475-68
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SOFTWARE: Patentin version 3.3
SEQ ID NO 356
LENGTH: 325
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Best Local S
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TYPE: PRT
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| Sequence 8, Application US/11012762 |
| Publication No. US20050244815A1 |
| GENERAL INFORMATION: GEODGIA State University Research Foundation, Inc. |
| APPLICANT: Georgia State University Research Foundation, Inc. |
| TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes |
| TILE OF INVENTION: Compositions and Methods for Viral Resistance Genes |
| FILE REFERENCE: GSUI PCT |
| CURRENT FILING DATE: 2004-12-15 |
| PRIOR APPLICATION NUMBER: US/11/012,762 |
| PRIOR APPLICATION NUMBER: US 60/390,046 |
| PRIOR FILING DATE: 2003-66-19 |
| NUMBER OF SEQ ID NOS: 133 |
| SOFTWARE: Patentin Version 3.2 |
| SEQ ID NO 8 |

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118 RQNEADGGWSLVITQRQDYETATMQSYVFSIQVEGESQAVLVALEIVN------ 165
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26.3%; Pred. No. 69;
tive 11; Mismatches 28; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.2%; Score 63; DB 7; Length 171'
Best Local Similarity 19.7%; Pred. No. 1.6e+02;
Matches 28; Conservative 24; Mismatches 52; Indels
PRIOR APPLICATION NUMBER: 2005-07-29
; PRIOR APPLICATION NUMBER: US/09/715,909
; PRIOR PILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/166,285
; PRIOR APPLICATION NUMBER: 60/166,285
; PRIOR APPLICATION NUMBER: 09911-18
; SEQ ID NOS: 11
; SOFTWARE: FASISEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1717
; TYPE: num
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215 SRAA-----DESIFYMVGEY 229
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Publication No. US20050250678A1
GRWERAL INFORMATION:
APPLICANT: Neose Technologies Inc.
APPLICANT: DeFrees, Shwm
APPLICANT: Zopf, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 FRKSKEKIGKEFKRIV 154
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736 GQEDKKKIKTESGRFI 751
                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Ostrinia nubilalis
US-11-193-715-2
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Best Local Similarity 26.3*
Conservative
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; ORGANISM: Mus musculus
US-11-012-762-8
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US-11-033-365-198
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69 GDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKD 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.1%; Score 62; DB 7; Length 192; Best Local Similarity 25.7%; Pred. No. 9.6; Matches 39; Conservative 24; Mismatches 37; Indels
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APPLICANT: Decree, Shawn
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Clausen, Henrik
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: O-Linked Glycosylation of peptides
FILE REFERENCE: 040853-01-5138
CURRENT APPLICATION NUMBER: US/11/033,365
CURRENT FILING DATE: 2005-01-10
PRIOR PELICATION NUMBER: 60/544,411
PRIOR PELICATION NUMBER: 60/544,411
PRIOR FILING DATE: 2004-01-08
PRIOR FILING DATE: 2004-02-02
PRIOR PELICATION NUMBER: 60/546,631
PRIOR FILING DATE: 2004-02-20
PRIOR FILING DATE: 2004-03-23
PRIOR FILING DATE: 2004-05-12
NUMBER OF SEQ ID NOS: 213
SOFTWARE: Patentin version 3.2
SEQ ID NO 200
LEMOTH: 192
APPLICANT: Mausy Mineraly
TITLE OF INVENTION: O-Linked Glycosylation of peptides
TITLE OF INVENTION: O-Linked Glycosylation of peptides
FILE REPERENCE: 040853-01-5138
CURRENT APPLICATION NUMBER: 05/11/033,365
CURRENT FILING DATE: 2005-01-10
FRIOR PELING DATE: 2004-01-08
FRIOR FILING DATE: 2004-02-12
FRIOR APPLICATION NUMBER: 60/546,631
FRIOR FILING DATE: 2004-02-20
FRIOR FILING DATE: 2004-02-20
FRIOR FILING DATE: 2004-02-30
FRIOR FILING DATE: 2004-03-33
FRIOR FILING DATE: 2004-03-33
FRIOR APPLICATION NUMBER: 60/55,813
FRIOR PELING DATE: 2004-05-12
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Publication No. US20050250678A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version
SEQ ID NO 198
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US-11-033-365-198
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US-11-033-365-200
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                                                                                14 SLVLLLLGLVMPLAIIAQVLSYKEAV--LRAI--DGINQRSSDANLYRLL-DLDP--RPT 66
                                           54; Gaps
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Best Local Similarity 21.9%; Pred. No. 18;
Matches 28; Conservative 28; Mismatches 60; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kleachammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Olivia
APPLICANT: Perll, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REPERBUCE: 5051-694
CURRENT FILING DATE: 2005-03-07
PRIOR PPLING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 362
LENGTH: 301
DB 7; Length 192;
  Query Match 7.1%; Score 62; DB 7; Length 192; Best Local Similarity 25.5%; Pred. No. 9.6; Matches 39; Conservative 23; Mismatches 37; Indels
                                                                                                                                                                                                126 MGRLEDGSPNTGQ----IFKQTYSKFDTNSHNDDALLKNYGL----
                                                                                                                                                                                                                                           123 ISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQ 155
                                                                                                                                                                                                                                                                  Search completed: January 12, 2006, 21:54:25 Job time : 8.52768 secs
                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 362, Application US/11074176; Publication No. US20050250135A1; GENERAL INFORMATION:
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; ORGANISM: Lactobacillus acidophilus
US-11-074-176-362
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259 SRKEIERL 266
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US-11-074-176-362
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Published_Applications Mucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published Applications applications.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions rupbm (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions rapbm (Published_Applications_AA_New).

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